

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2001, 23:56:33 ; Search time 1171.01 Seconds
(without alignments)
6989.746 Million cell updates/sec

Title: US-09-382-242-23

Perfect score: 555
Sequence: 1 ATGCTTTAAACAGCACTC.....AATCATACACTAACGATAG 555

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1283235 segs, 7373929652 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- GenEmb1:*
- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
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- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_rol:*
- 95: gb_rol2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	4.1	80376	12 AB010073	AB010073 Arabidops
2	22	4.0	133137	86 AC007245	AC007245 Homo sapi
3	22	4.0	151429	68 AC023570	AC023570 Homo sapi
4	22	4.0	172127	63 AC012690	AC012690 Homo sapi
5	20	3.6	348	92 HSATP7A06	U27365 Human Menke
6	20	3.6	403	92 HSMDG6	X82340 Homo sapien
7	20	3.6	52946	5 CELR04A9	U41550 Caenorhabdi
8	20	3.6	74432	91 HS465G10B	Z94801 Human DNA S
9	20	3.6	87022	82 AP001089	AP001089 Homo sapi
10	20	3.6	132749	60 AC006778	AC006778 Caenorhab
11	20	3.6	142362	72 AC036162	AC036162 Homo sapi

C	12	20	3.6	155172	66	AC021110	Homo sapi	C	85	18	3.2	3124	2	AF270088	AF270088	Staphyloc
C	13	20	3.6	155261	62	AC011921	Homo sapi	C	86	18	3.2	3140	59	HSEUNGS	L33971	Cottontail
C	14	20	3.6	159999	79	AL161417	Homo sapi	C	87	18	3.2	3211	88	AK000288	AK000288	Homo sapi
C	15	20	3.6	164746	69	AC025515	Homo sapi	C	88	18	3.2	3643	2	AF270154	AF270154	Staphyloc
C	16	20	3.6	174815	82	AP001390	Homo sapi	C	89	18	3.2	4571	85	AB051531	AB051531	Homo sapi
C	17	20	3.6	183836	79	AL163544	Homo sapi	C	90	18	3.2	7736	3	STH242480	STH242480	Streptococ
C	18	20	3.6	202553	61	AC009774	Homo sapi	C	91	18	3.2	12900	4	AE001429	AE001429	Plasmodu
C	19	19	3.4	385	2	CPDHAT	X86487	C	92	18	3.2	22000	14	SPC229	SPC229	S. pombe
C	20	19	3.4	430	5	AF202766	Artemia p	C	93	18	3.2	24128	77	AC084416	AC084416	Continuatio
C	21	19	3.4	430	5	AF202767	Artemia p	C	94	18	3.2	34617	12	AC004625	AC004625	(5 of
C	22	19	3.4	430	5	AF202768	Artemia p	C	95	18	3.2	39101	14	SPAC5747	SPAC5747	AC004625
C	23	19	3.4	430	5	AF202769	Artemia p	C	96	18	3.2	42022	15	YSC19449	YSC19449	293396
C	24	19	3.4	430	5	AF202770	Artemia p	C	97	18	3.2	44410	4	AC084268	AC084268	S. pombe
C	25	19	3.4	2213	94	AF035207	Mus muscu	C	98	18	3.2	54676	66	AC020213	AC020213	Caenorhab
C	26	19	3.4	2940	94	AF153350	Mus muscu	C	99	18	3.2	57327	94	AC030318	AC030318	AC020213
C	27	19	3.4	9085	85	AB009808	Mus muscu	C	100	18	3.2	58943	70	AC025850	AC025850	Mus muscu
C	28	19	3.4	14230	93	HUMTCM1A	M86360	C	101	18	3.2	60153	69	AC025498	AC025498	AC025498
C	29	19	3.4	14537	93	HUMKERTRA	M99447	C	102	18	3.2	64650	74	AC068864	AC068864	AC025498
C	30	19	3.4	16388	3	U32830	H94447	C	103	18	3.2	71806	78	AC087464	AC087464	AC068864
C	31	19	3.4	50334	92	HS995012	U32830	C	104	18	3.2	74690	67	AC022581	AC022581	AC087464
C	32	19	3.4	71532	68	AC074230	AL035462	C	105	18	3.2	80689	4	AC003053	AC003053	AC022581
C	33	19	3.4	92004	76	AC074230	AL035462	C	106	18	3.2	81293	12	AB018109	AB018109	AC003053
C	34	19	3.4	93418	81	AL390955	AL390955	C	107	18	3.2	89004	6	CEY6982	CEY6982	AB018109
C	35	19	3.4	114956	85	AC002072	AC002072	C	108	18	3.2	89934	12	AC007067	AC007067	Caenorhabd
C	36	19	3.4	116448	12	AC005142	AC005142	C	109	18	3.2	91916	12	AC005964	AC005964	Genomic s
C	37	19	3.4	139399	13	AP002865	AP002865	C	110	18	3.2	92918	66	AC020050	AC020050	AC005964
C	38	19	3.4	140210	60	AC002993	AP002865	C	111	18	3.2	97348	94	AF091216	AF091216	AC020050
C	39	19	3.4	145174	88	AF289077	AF289077	C	112	18	3.2	98070	88	AC025463	AC025463	AC091216
C	40	19	3.4	147310	82	AL513495	AL113495	C	113	18	3.2	98119	83	HSN15446	HSN15446	AC025463
C	41	19	3.4	150336	92	HS7395C13	AL117344	C	114	18	3.2	98491	94	AF132039	AF132039	AC091216
C	42	19	3.4	155876	79	AL354809	AL154809	C	115	18	3.2	100605	78	AC087157	AC087157	AC025463
C	43	19	3.4	156780	77	AC083838	AC083838	C	116	18	3.2	102049	83	CEY51A2_3	CEY51A2_3	AF132039
C	44	19	3.4	157090	85	AB019441	AB019441	C	117	18	3.2	106636	76	AC079437	AC079437	Mus muscu
C	45	19	3.4	159029	71	AC027201	AC027201	C	118	18	3.2	107484	91	HS424116	HS424116	Continuatio
C	46	19	3.4	159629	13	ATCHRIV9	AL161497	C	119	18	3.2	108581	69	AC025458	AC025458	(4 of
C	47	19	3.4	159716	70	AC025807	AC025807	C	120	18	3.2	108634	66	AC020813	AC020813	AL034373
C	48	19	3.4	163797	70	AC025872	AC025872	C	121	18	3.2	109508	89	AL133329	AL133329	AC025458
C	49	19	3.4	166758	85	AC003046	AC003046	C	122	18	3.2	110000	75	AC073702	AC073702	Mus muscu
C	50	19	3.4	167172	87	AC009428	AC009428	C	123	18	3.2	110000	75	AC073702	AC073702	Continuatio
C	51	19	3.4	167977	81	AL451129	AL451129	C	124	18	3.2	110000	75	AC073804	AC073804	(2 of
C	52	19	3.4	169383	69	AC024291	AC024291	C	125	18	3.2	110000	75	AC073804	AC073804	Continuatio
C	53	19	3.4	171038	90	AP001598	AP001598	C	126	18	3.2	110000	75	AC073804	AC073804	(2 of
C	54	19	3.4	171267	72	AC040979	AC040979	C	127	18	3.2	110000	77	AC073804	AC073804	Continuatio
C	55	19	3.4	171502	72	AC046152	AC046152	C	128	18	3.2	110312	94	AF131866	AF131866	(3 of
C	56	19	3.4	172596	61	AC009707	AC009707	C	129	18	3.2	110680	12	AC006259	AC006259	Continuatio
C	57	19	3.4	174768	76	AC079191	AC079191	C	130	18	3.2	111775	94	AC018559	AC018559	(2 of
C	58	19	3.4	174798	79	AL157889	AL157889	C	131	18	3.2	113249	74	AC068805	AC068805	Continuatio
C	59	19	3.4	176594	66	AC020983	AC020983	C	132	18	3.2	113547	62	AC011346	AC011346	(2 of
C	60	19	3.4	176530	78	AC087156	AC087156	C	133	18	3.2	115049	75	AC073746	AC073746	Continuatio
C	61	19	3.4	176623	87	AC0113429	AC0113429	C	134	18	3.2	115049	75	AC073746	AC073746	Continuatio
C	62	19	3.4	180493	62	AC011189	AC011189	C	135	18	3.2	115049	75	AC073746	AC073746	Continuatio
C	63	19	3.4	182756	12	AC007789	AC007789	C	136	18	3.2	115173	63	AC012612	AC012612	Mus muscu
C	64	19	3.4	182751	68	AC023098	AC023098	C	137	18	3.2	120397	76	AC079465	AC079465	Continuatio
C	65	19	3.4	185171	68	AC023098	AC023098	C	138	18	3.2	120397	76	AC079465	AC079465	Continuatio
C	66	19	3.4	194810	69	AC024984	AC024984	C	139	18	3.2	121063	76	AC079482	AC079482	Continuatio
C	67	19	3.4	196530	83	CNS00YVI	AL096870	C	140	18	3.2	122049	92	HSB166C10	HSB166C10	Mus muscu
C	68	19	3.4	199132	81	AL512631	AL512631	C	141	18	3.2	122236	77	AC079884	AC079884	Continuatio
C	69	19	3.4	203269	77	AC084876	AC084876	C	142	18	3.2	122236	77	AC079884	AC079884	Continuatio
C	70	19	3.4	204557	81	AL512585	AL512585	C	143	18	3.2	122236	14	IS002M01	IS002M01	Mus muscu
C	71	19	3.4	208306	83	CNS01DSC	AL121767	C	144	18	3.2	132169	70	AC026814	AC026814	Continuatio
C	72	19	3.4	210772	63	AC012215	AC012215	C	145	18	3.2	134350	85	AC004905	AC004905	Mus muscu
C	73	19	3.4	214341	77	CNS01DRT	AL118557	C	146	18	3.2	136862	85	AC005007	AC005007	Continuatio
C	74	19	3.4	216315	92	HSG256022	AC084163	C	147	18	3.2	137953	77	AC083888	AC083888	Continuatio
C	75	19	3.4	226059	76	AC079488	AL080239	C	148	18	3.2	137953	77	AC083888	AC083888	Continuatio
C	76	19	3.4	303041	67	AC029435	AL080239	C	149	18	3.2	138970	70	AC026679	AC026679	Continuatio
C	77	19	3.4	306200	2	AP000991	AC029488	C	150	18	3.2	145976	87	AC087130	AC087130	Continuatio
C	78	19	3.4	312615	75	AC073722	AC073722	C	151	18	3.2	147006	84	SPEN01904	SPEN01904	Mus muscu
C	79	19	3.4	340000	90	AP001697	AP001697	C	152	18	3.2	147744	61	AC008856	AC008856	Continuatio
C	80	18	3.2	527	53	CNS01RHY	AL144455	C	153	18	3.2	148042	88	AC034226	AC034226	Continuatio
C	81	18	3.2	1356	14	SCYLRO79W	AL144455	C	154	18	3.2	148648	73	AC068120	AC068120	Continuatio
C	82	18	3.2	1798	12	SCYLRO869	Z73251	C	155	18	3.2	149313	68	AC023548	AC023548	Continuatio
C	83	18	3.2	2537	14	SCYLRO80W	AF033869	C	156	18	3.2	150695	68	AC023548	AC023548	Continuatio
C	84	18	3.2	2845	94	AB023433	Z73252	C	157	18	3.2	151104	61	AC010250	AC010250	Continuatio

c 158	18	3.2 151212	77	AC079885	AC079885	Rattus no	231	18	3.2 181596	74	AC069467	AC069467	Mus muscu
c 159	18	3.2 151788	78	AF321234	AF321234	Mus muscu	232	18	3.2 182421	65	AC016742	AC016742	Hom sapl
c 160	18	3.2 151959	62	AC011153	AC011153	Hom sapl	c 233	18	3.2 182982	72	AC036231	AC036231	Hom sapl
c 161	18	3.2 151979	69	AC025113	AC025113	Hom sapl	234	18	3.2 183042	81	AL445529	AL445529	Hom sapl
c 162	18	3.2 152468	82	AP001584	AP001584	Hom sapl	235	18	3.2 183936	94	AC079798	AC079798	Mus muscu
c 163	18	3.2 152544	68	AC023508	AC023508	Mus muscu	236	18	3.2 184000	64	AC016595	AC016595	Mus muscu
c 164	18	3.2 152742	67	AC022381	AC022381	Hom sapl	c 237	18	3.2 184161	71	AC027646	AC027646	Mus muscu
c 165	18	3.2 153027	71	AC027300	AC027300	Mus muscu	c 238	18	3.2 185351	87	AC015801	AC015801	Hom sapl
c 166	18	3.2 153258	70	AC026206	AC026206	Hom sapl	c 239	18	3.2 185462	98	AC087775	AC087775	Mus muscu
c 167	18	3.2 153433	70	AC026033	AC026033	Hom sapl	240	18	3.2 185548	74	AC005743	AC005743	Mus muscu
c 168	18	3.2 154704	2	AP000996	AP000996	Thermopla	c 241	18	3.2 185637	60	AC007979	AC007979	Mus muscu
c 169	18	3.2 155313	62	AC011091	AC011091	Hom sapl	242	18	3.2 186415	86	AC008675	AC008675	Mus muscu
c 170	18	3.2 155653	69	AC023510	AC023510	Hom sapl	c 243	18	3.2 186420	87	AC018757	AC018757	Hom sapl
c 171	18	3.2 155827	83	CNS05FC1	AL355099	Hom sapl	244	18	3.2 187376	73	AC068352	AC068352	Mus muscu
c 172	18	3.2 156266	13	AP002542	AP002542	Oryza sat	c 245	18	3.2 188750	94	AC078931	AC078931	Mus muscu
c 173	18	3.2 157180	14	NCB18D24	AL513466	Neurospor	c 246	18	3.2 189397	72	AC051643	AC051643	Mus muscu
c 174	18	3.2 157258	86	AC008379	AC008379	Hom sapl	c 247	18	3.2 190559	77	AC084164	AC084164	Mus muscu
c 175	18	3.2 157665	94	AC069018	AC069018	Mus muscu	248	18	3.2 190737	78	AL136158	AL136158	Mus muscu
c 176	18	3.2 157944	61	AC008788	AC008788	Hom sapl	c 249	18	3.2 191289	76	AC079290	AC079290	Mus muscu
c 177	18	3.2 158442	76	AC078920	AL359999	Hom sapl	c 250	18	3.2 191352	75	AC073565	AC073565	Mus muscu
c 178	18	3.2 158853	80	AL359999	AC056118	Hom sapl	251	18	3.2 191998	75	AC073869	AC073869	Hom sapl
c 179	18	3.2 160376	72	AC036118	AC023129	Hom sapl	252	18	3.2 192015	67	AC022453	AC022453	Mus muscu
c 180	18	3.2 161696	68	AC023129	AC023129	Hom sapl	c 253	18	3.2 193185	68	AC023606	AC023606	Mus muscu
c 181	18	3.2 163154	81	AL365196	AL365196	Hom sapl	c 254	18	3.2 193488	89	AL136097	AL136097	Human DNA
c 182	18	3.2 163328	64	AC016190	AC016190	Hom sapl	255	18	3.2 193636	76	AC079428	AC079428	Mus muscu
c 183	18	3.2 163449	76	AC078896	AC078896	Mus muscu	c 256	18	3.2 193708	76	AC074205	AC074205	Mus muscu
c 184	18	3.2 163860	67	AC021628	AC021628	Mus muscu	257	18	3.2 193907	78	AC087131	AC087131	Mus muscu
c 185	18	3.2 164119	70	AC026640	AC026640	Hom sapl	258	18	3.2 194262	81	AL450406	AL450406	Mus muscu
c 186	18	3.2 164682	73	AC064801	AC064801	Hom sapl	c 259	18	3.2 194394	72	AC040934	AC040934	Mus muscu
c 187	18	3.2 164816	67	AC022011	AC022011	Hom sapl	260	18	3.2 194476	75	AC074177	AC074177	Hom sapl
c 188	18	3.2 165372	72	AC051613	AC051613	Mus muscu	c 261	18	3.2 194985	94	AC023406	AC023406	Mouse chr
c 189	18	3.2 165549	89	AL355498	AL355498	Human DNA	c 262	18	3.2 195090	68	AC023150	AC023150	Hom sapl
c 190	18	3.2 165776	81	AL500524	AL500524	Hom sapl	263	18	3.2 195423	13	AC087151	AC087151	Mus muscu
c 191	18	3.2 166335	75	AC073799	AC073799	Mus muscu	c 264	18	3.2 196149	78	AC087151	AC087151	Mus muscu
c 192	18	3.2 167829	61	AC008858	AC008858	Hom sapl	c 265	18	3.2 197571	66	AC021042	AC021042	Mus muscu
c 193	18	3.2 167998	65	AC018835	AC018835	Hom sapl	c 266	18	3.2 198181	72	AC035248	AC035248	Mus muscu
c 194	18	3.2 168015	70	AC026000	AC026000	Hom sapl	c 267	18	3.2 198515	94	AF129005	AF129005	Mus muscu
c 195	18	3.2 168224	68	AC022976	AC022976	Hom sapl	c 268	18	3.2 198564	75	AC073939	AC073939	Mus muscu
c 196	18	3.2 168346	72	AC036227	AC036227	Hom sapl	269	18	3.2 198601	81	AL450395	AL450395	Mus muscu
c 197	18	3.2 168359	77	AC079816	AC079816	Mus muscu	c 270	18	3.2 199100	74	AC068902	AC068902	Mus muscu
c 198	18	3.2 168457	76	AC078913	AC078913	Mus muscu	c 271	18	3.2 199256	75	AC073553	AC073553	Mus muscu
c 199	18	3.2 170356	94	AF259072	AF259072	Mus muscu	c 272	18	3.2 199364	77	AC080064	AC080064	Mus muscu
c 200	18	3.2 170695	74	AC068545	AC068545	Hom sapl	c 273	18	3.2 200000	60	AC007117	AC007117	Hom sapl
c 201	18	3.2 172440	73	AC068234	AC068234	Hom sapl	c 274	18	3.2 200161	76	AC074313	AC074313	Mus muscu
c 202	18	3.2 173088	62	AC011170	AC011170	Hom sapl	c 275	18	3.2 200492	63	AC012117	AC012117	Mus muscu
c 203	18	3.2 173735	71	AC027063	AC027063	Hom sapl	c 276	18	3.2 200588	82	AL513206	AL513206	Hom sapl
c 204	18	3.2 174639	88	AC026214	AC026214	Hom sapl	c 277	18	3.2 201015	61	AC010075	AC010075	Mus muscu
c 205	18	3.2 174663	88	AC087092	AC087092	Hom sapl	c 278	18	3.2 201615	76	AC079274	AC079274	Mus muscu
c 206	18	3.2 175093	71	AC027185	AC027185	Mus muscu	c 279	18	3.2 202333	77	AC080144	AC080144	Mus muscu
c 207	18	3.2 175144	74	AC068502	AC068502	Mus muscu	c 280	18	3.2 202640	68	AC023234	AC023234	Mus muscu
c 208	18	3.2 175331	76	AC079275	AC079275	Mus muscu	c 281	18	3.2 202894	67	AC021630	AC021630	Mus muscu
c 209	18	3.2 176155	66	AC020879	AC020879	Mus muscu	c 282	18	3.2 202912	74	AC069560	AC069560	Mus muscu
c 210	18	3.2 176506	77	AC079956	AC079956	Mus muscu	c 283	18	3.2 203349	73	AC055819	AC055819	Mus muscu
c 211	18	3.2 176564	70	AC026367	AC026367	Hom sapl	c 284	18	3.2 203959	90	AP001137	AP001137	Hom sapl
c 212	18	3.2 176853	70	AC026335	AC026335	Hom sapl	c 285	18	3.2 204056	89	AL160397	AL160397	Human DNA
c 213	18	3.2 177130	66	AC019351	AC019351	Hom sapl	c 286	18	3.2 205104	81	AL391989	AL391989	Hom sapl
c 214	18	3.2 177205	76	AC079217	AC079217	Mus muscu	c 287	18	3.2 205677	74	AC068651	AC068651	Mus muscu
c 215	18	3.2 177663	75	AC074129	AC074129	Hom sapl	c 288	18	3.2 205959	67	AC022328	AC022328	Mus muscu
c 216	18	3.2 177663	75	AC074129	AC074129	Hom sapl	c 289	18	3.2 205992	72	AC044811	AC044811	Mus muscu
c 217	18	3.2 177751	65	AC016844	AC016844	Hom sapl	c 290	18	3.2 206383	94	AC008160	AC008160	Mus muscu
c 218	18	3.2 177767	70	AC026384	AC026384	Mus muscu	c 291	18	3.2 206703	77	AC083909	AC083909	Mus muscu
c 219	18	3.2 177767	87	AC026384	AC026384	Mus muscu	c 292	18	3.2 206703	77	AC083909	AC083909	Mus muscu
c 220	18	3.2 177803	87	AC010411	AC010411	Hom sapl	c 293	18	3.2 207607	75	AC073590	AC073590	Mus muscu
c 221	18	3.2 177914	87	AC080141	AC080141	Mus muscu	c 294	18	3.2 207949	71	AC027497	AC027497	Hom sapl
c 222	18	3.2 178180	87	AC008770	AC008770	Hom sapl	c 295	18	3.2 208211	77	AC084287	AC084287	Mus muscu
c 223	18	3.2 178509	78	AL137069	AL137069	Hom sapl	c 296	18	3.2 208211	77	AC084287	AC084287	Mus muscu
c 224	18	3.2 179272	74	AC069149	AC069149	Hom sapl	c 297	18	3.2 208295	69	AC025528	AC025528	Mus muscu
c 225	18	3.2 179452	81	AL512586	AL512586	Mus muscu	c 298	18	3.2 208405	81	AL365219	AL365219	Hom sapl
c 226	18	3.2 179493	70	AC026683	AC026683	Mus muscu	c 299	18	3.2 208910	76	AC079573	AC079573	Mus muscu
c 227	18	3.2 179581	61	AC009397	AC009397	Hom sapl	c 300	18	3.2 208910	76	AC079573	AC079573	Mus muscu
c 228	18	3.2 180548	77	AC083884	AC083884	Hom sapl	c 301	18	3.2 208932	76	AC074329	AC074329	Mus muscu
c 229	18	3.2 181008	76	AC079219	AC079219	Mus muscu	c 302	18	3.2 209301	76	AC079529	AC079529	Mus muscu
c 230	18	3.2 181179	89	AL161725	AL161725	Human DNA	c 303	18	3.2 211600	63	AC013266	AC013266	Hom sapl

304	18	3.2	211615	71	AC026949	Mus muscu	c	377	17	3.1	816	14	CRPSAH	X15164 C.reinhardt	
c	305	18	3.2	212437	79	AL354924	Homo sapi	378	17	3.1	902	53	CNS01R72	AL157038 Anopheles	
306	18	3.2	212658	76	AC079426	Mus muscu	379	17	3.1	1011	53	CNS0719P	AL42643 T3 end of		
307	18	3.2	213296	73	AC067784	Homo sapi	380	17	3.1	1147	75	AC073605	AK023605 Homo sapi		
308	18	3.2	213308	76	AC079164	Mus muscu	381	17	3.1	1160	89	AK026210	AK026210 Homo sapi		
309	18	3.2	213318	72	AC036121	Mus muscu	382	17	3.1	1360	89	AK026210	AK026210 Homo sapi		
310	18	3.2	214157	76	AC079511	Mus muscu	383	17	3.1	1521	89	AK021466	AK021466 Homo sapi		
c	311	18	3.2	214157	76	AC079511	Mus muscu	384	17	3.1	1660	9	AX028832	AX028832 Sequence	
312	18	3.2	214707	73	AC073945	Mus muscu	c	384	17	3.1	2134	11	PT4DDAA	J05172 Bacterioph	
313	18	3.2	215309	75	AC060761	Mus muscu	c	385	17	3.1	2255	14	PSAPSPYN2	Y13322 Plasm sativ	
c	314	18	3.2	215309	75	AC060761	Mus muscu	c	385	17	3.1	2368	94	MMU251508	Y135251508 Mus muscu
c	315	18	3.2	216101	81	AL450331	Mus muscu	c	386	17	3.1	2426	89	AK026452	AK026452 Homo sapi
c	316	18	3.2	216340	75	AC073754	Mus muscu	c	387	17	3.1	2590	7	AF222767	AF222767 Homo sapi
c	316	18	3.2	216583	78	AC087166	Mus muscu	c	388	17	3.1	2674	93	SSCFMR7	AF222767 Bos tauru
c	317	18	3.2	217250	65	AC018595	Mus muscu	c	389	17	3.1	2676	92	HSMB01876	AF222767 S.claureus
c	318	18	3.2	218907	78	AC087558	Homo sapi	c	390	17	3.1	3263	6	DRODLGA	AL136908 Homo sapi
319	18	3.2	220469	76	AC074307	Mus muscu	c	391	17	3.1	3263	6	DRODLGA	AL136908 Homo sapi	
c	320	18	3.2	221111	76	AC079526	Mus muscu	c	392	17	3.1	4011	14	PSADH1	X06281 Pea mRNA fo
c	321	18	3.2	221285	68	AC023611	Mus muscu	c	393	17	3.1	4055	13	AF216457	AF224697 Gossypium
322	18	3.2	221478	76	AC079545	Mus muscu	c	394	17	3.1	4073	2	CBORNTF	X62622 C.barati ge	
323	18	3.2	222468	76	AC079525	Mus muscu	c	395	17	3.1	4148	93	HUM21DC922	L48476 Homo sapien	
c	324	18	3.2	222468	76	AC079525	Mus muscu	c	396	17	3.1	4938	3	SYPSAAB	X58825 Synchocyst
325	18	3.2	222658	94	AC055766	Mus muscu	c	397	17	3.1	6536	4	AE002878	AE002878 Drosophila	
c	326	18	3.2	222707	76	AC079425	Mus muscu	c	398	17	3.1	6731	85	AB007967	AB007967 Homo sapi
c	327	18	3.2	226168	94	AC078930	Mus muscu	c	399	17	3.1	6850	5	CEIC13E3	U40936 Caenorhabdi
c	328	18	3.2	228667	81	AL365336	Mus muscu	c	400	17	3.1	7348	58	ECR5695	U40936 Caenorhabdi
c	329	18	3.2	228789	72	AC051638	Mus muscu	c	401	17	3.1	7721	94	AF003255	AF003255 Mus muscu
c	330	18	3.2	229010	75	AC073686	Mus muscu	c	402	17	3.1	7764	66	AC019416	AC019416 Drosophila
c	331	18	3.2	229010	75	AC073686	Mus muscu	c	403	17	3.1	8127	1	AB007122	AB007122 Arthropac
c	332	18	3.2	230693	80	AL359352	Mus muscu	c	404	17	3.1	8682	14	CIP345R5S	L10215 Mesembryant
c	333	18	3.2	231709	74	AC068561	Mus muscu	c	405	17	3.1	10563	3	U39682	U39682 Mycoplasma
c	334	18	3.2	234257	76	AC079574	Mus muscu	c	406	17	3.1	11198	1	AE006271	AE006271 Lactocococ
c	335	18	3.2	234411	94	MMU2971	Mus muscu	c	407	17	3.1	11261	93	HSFMP03	U56088 Human perlo
c	336	18	3.2	239423	77	AC083912	Mus muscu	c	408	17	3.1	11698	2	KOCYMSCGT	X86014 K.oxyloca c
c	337	18	3.2	240622	75	AC073793	Mus muscu	c	409	17	3.1	15121	6	LMFL6754	AL358632 Leishman
c	338	18	3.2	244110	82	AL513022	Mus muscu	c	410	17	3.1	15859	5	CEFO7D3	Z71179 Caenorhabdi
c	339	18	3.2	244215	75	AC073706	Mus muscu	c	411	17	3.1	20981	65	AC017212	AC017212 Drosophila
c	340	18	3.2	244215	75	AC073706	Mus muscu	c	412	17	3.1	26147	5	CEZC101	Z93395 Caenorhabdi
c	341	18	3.2	245156	77	AC084021	Mus muscu	c	413	17	3.1	26703	6	CEBKG45011	AC084652 Caenorhab
c	342	18	3.2	246823	76	AC079483	Mus muscu	c	414	17	3.1	26767	6	CELMU07G9	AF040658 Caenorhab
c	343	18	3.2	251216	76	AC079558	Mus muscu	c	415	17	3.1	32410	90	AP000164	AP000164 Homo sapi
c	344	18	3.2	251216	76	AC079558	Mus muscu	c	416	17	3.1	32588	6	CEY22E5A	AL021479 Caenorhab
c	345	18	3.2	252504	75	AC073815	Mus muscu	c	417	17	3.1	34338	66	AC020840	AC020840 Mus muscu
c	346	18	3.2	254475	69	AC025117	Mus muscu	c	418	17	3.1	35740	88	AF199339	AF199339 Homo sapi
c	347	18	3.2	256673	78	AC087146	Mus muscu	c	419	17	3.1	36080	6	CER10D12	Z81109 Caenorhabdi
c	348	18	3.2	258088	75	AC073766	Mus muscu	c	420	17	3.1	36992	93	HSU73640	Z81109 Caenorhabdi
c	349	18	3.2	262205	4	AE003647	Mus muscu	c	421	17	3.1	38591	5	CEC54E10	U73640 Human chrom
c	350	18	3.2	276523	94	AC012382	Mus muscu	c	422	17	3.1	40033	91	HS1110P6	Z81047 Caenorhabdi
c	351	18	3.2	291768	76	AC074229	Mus muscu	c	423	17	3.1	40289	92	CEX48610A	AL132917 Human DNA
c	352	18	3.2	292943	68	AC023605	Mus muscu	c	424	17	3.1	42807	92	HSJ309F20	AL121917 Human DNA
c	353	18	3.2	292943	68	AC023605	Mus muscu	c	425	17	3.1	43051	85	AB001517	AB001517 Homo sapi
c	354	18	3.2	293184	76	AC079487	Mus muscu	c	426	17	3.1	43125	5	AF147779	AF147779 Drosophila
c	355	18	3.2	293184	76	AC079487	Mus muscu	c	427	17	3.1	44499	12	AB016876	AB016876 Arabidops
c	356	18	3.2	299574	76	AC079512	Mus muscu	c	428	17	3.1	45794	64	AC015492	AC015492 Homo sapi
c	357	18	3.2	300250	94	AF125314	Mus muscu	c	429	17	3.1	46778	77	AC079784	AC079784 Homo sapi
c	358	18	3.2	303249	2	AE001515	Mus muscu	c	430	17	3.1	47743	5	CELC06E2	U39674 Caenorhabdi
c	359	18	3.2	304383	4	AE003579	Mus muscu	c	431	17	3.1	47743	5	CELC06E2	U39674 Caenorhabdi
c	359	18	3.2	304407	75	AC073813	Mus muscu	c	432	17	3.1	48008	12	AB025621	AB025621 Arabidops
c	360	18	3.2	307380	78	AC087155	Mus muscu	c	433	17	3.1	48823	65	AC017217	AC017217 Drosophila
c	361	18	3.2	312430	3	REPXX02	Mus muscu	c	434	17	3.1	50191	90	AL450471	AL450471 Human DNA
c	362	18	3.2	312615	75	AC073722	Mus muscu	c	435	17	3.1	52290	69	AC025314	AC025314 Homo sapi
c	363	18	3.2	316756	65	DROSADH06	Mus muscu	c	436	17	3.1	53444	66	AC019747	AC019747 Drosophila
c	364	18	3.2	318503	75	AC074166	Mus muscu	c	437	17	3.1	53635	78	AC087498	AC087498 Homo sapi
c	365	18	3.2	331339	66	AC020958	Mus muscu	c	438	17	3.1	57186	85	AC004042	AC004042 Homo sapi
c	366	18	3.2	340000	90	AP001681	Mus muscu	c	439	17	3.1	60309	78	AL138922	AL138922 Homo sapi
c	367	17	3.1	299	54	G26916	Mus muscu	c	440	17	3.1	63442	66	AC020280	AC020280 Drosophila
c	368	17	3.1	388	5	AF058227	Mus muscu	c	441	17	3.1	63682	78	AL135782	AL135782 Homo sapi
c	369	17	3.1	393	5	AF072664	Mus muscu	c	442	17	3.1	65771	63	AC013600	AC013600 Homo sapi
c	370	17	3.1	431	54	AF072664	Mus muscu	c	443	17	3.1	65848	91	HS892F13	AL1009183 Human DNA
c	371	17	3.1	649	2	MCU02253	Mus muscu	c	444	17	3.1	65971	63	AC013231	AC013231 Drosophila
c	372	17	3.1	652	54	GS3107	Mus muscu	c	445	17	3.1	66452	69	AC024328	AC024328 Homo sapi
c	373	17	3.1	660	14	CNS01C02	Mus muscu	c	446	17	3.1	66806	90	AP000022	AP000022 Homo sapi
c	374	17	3.1	720	14	CNS01C03	Mus muscu	c	447	17	3.1	67249	65	AC018611	AC018611 Homo sapi
c	375	17	3.1	777	10	EL16701	Mus muscu	c	448	17	3.1	69463	77	AC084249	AC084249 Homo sapi
c	376	17	3.1	785	53	CNS077FM	Mus muscu	c	449	17	3.1	69614	77	AC083925	AC083925 Homo sapi
c	376	17	3.1	785	53	CNS077FM	Mus muscu	c	449	17	3.1	69714	69	AC024143	AC024143 Mus muscu

450	17	3.1	70768	12	AC007069	AC007069 Arabidops	523	17	3.1	114521	89	AL159985	AL159985 Human DNA
451	17	3.1	71801	79	AL153613	Continuation (4 of	524	17	3.1	115039	91	HS14588	AL035451 Human DNA
C 452	17	3.1	73166	77	AC083961	Continuation (4 of	C 525	17	3.1	117553	82	AP000595	AP000595 Homo sapi
C 453	17	3.1	73639	73	AC05834	Homo sapi	C 526	17	3.1	117937	78	AL139146	AL139146 Homo sapi
C 454	17	3.1	73947	90	AL445248	AL445248 Homo sapi	C 527	17	3.1	118421	82	AL133221	AL133221 Homo sapi
C 455	17	3.1	76339	89	AL157694	AL157694 Homo sapi	C 528	17	3.1	119072	89	AL136531	AL136531 Homo sapi
C 456	17	3.1	77223	90	AL160180	AL160180 Human DNA	C 529	17	3.1	120400	78	AL139106	AL139106 Homo sapi
C 457	17	3.1	78373	70	AC026519	AC026519 Homo sapi	C 530	17	3.1	120507	89	AL136358	AL136358 Homo sapi
C 458	17	3.1	79134	67	AC021771	AC021771 Homo sapi	C 531	17	3.1	123010	61	AC009746	AC009746 Homo sapi
C 459	17	3.1	79134	67	AC021771	AC021771 Homo sapi	C 532	17	3.1	123323	90	AP001816	AP001816 Homo sapi
C 460	17	3.1	79725	12	AC003105	AC003105 Arabidops	C 533	17	3.1	124343	76	AC079188	AC079188 Homo sapi
C 461	17	3.1	80201	61	AC009015	AC009015 Homo sapi	C 534	17	3.1	125441	61	AC008902	AC008902 Homo sapi
C 462	17	3.1	81266	12	AC006920	AC006920 Arabidops	C 535	17	3.1	125536	60	AL135679	AL135679 Homo sapi
C 463	17	3.1	81524	92	HS4J9616	HS4J9616 Homo sapi	C 536	17	3.1	126244	80	AL156779	AL156779 Homo sapi
C 464	17	3.1	82213	79	AL162264	AL162264 Homo sapi	C 537	17	3.1	126781	64	AC016375	AC016375 Homo sapi
C 465	17	3.1	82381	13	ATF27619	ATF27619 Arabidops	C 538	17	3.1	126814	61	AC008961	AC008961 Homo sapi
C 466	17	3.1	83057	90	AL445703	AL445703 Human DNA	C 539	17	3.1	126910	86	AC005556	AC005556 Homo sapi
C 467	17	3.1	83351	12	AC010657	AC010657 Genomic s	C 540	17	3.1	127413	89	AL137784	AL137784 Human DNA
C 468	17	3.1	83369	13	ATT30A10	ATT30A10 Arabidops	C 541	17	3.1	127646	86	AC008171	AC008171 Homo sapi
C 469	17	3.1	83371	13	ATTM4122	ATTM4122 Arabidops	C 542	17	3.1	127926	61	AC010337	AC010337 Homo sapi
C 470	17	3.1	83689	12	AB017067	AB017067 Arabidops	C 543	17	3.1	128265	60	AC007826	AC007826 Homo sapi
C 471	17	3.1	84371	82	AP001963	AP001963 Homo sapi	C 544	17	3.1	128921	88	AC068658	AC068658 Homo sapi
C 472	17	3.1	85559	68	AC022892	AC022892 Homo sapi	C 545	17	3.1	130177	92	HSBG279B7	HSBG279B7 Homo sapi
C 473	17	3.1	85757	4	AC001652	AC001652 Drosophill	C 546	17	3.1	131355	78	AC089989	AC089989 Homo sapi
C 474	17	3.1	86671	12	AC005724	AC005724 Arabidops	C 547	17	3.1	133258	85	AC004944	AC004944 Homo sapi
C 475	17	3.1	87110	91	HS438L4	HS438L4 Human DNA s	C 548	17	3.1	133478	85	AC004686	AC004686 Homo sapi
C 476	17	3.1	87114	85	AC005353	AC005353 Homo sapi	C 549	17	3.1	133787	87	AC015540	AC015540 Homo sapi
C 477	17	3.1	87306	78	AF205591	AF205591 Homo sapi	C 550	17	3.1	134189	76	AC079550	AC079550 Homo sapi
C 478	17	3.1	87402	90	AP001426	AP001426 Homo sapi	C 551	17	3.1	134515	91	HS354U5	HS354U5 Homo sapi
C 479	17	3.1	87619	64	AC016504	AC016504 Homo sapi	C 552	17	3.1	134649	85	AC004047	AC004047 Homo sapi
C 480	17	3.1	87925	85	AC005318	AC005318 Homo sapi	C 553	17	3.1	135095	77	AC084714	AC084714 Homo sapi
C 481	17	3.1	89319	92	HSBK29F11	AL118516 Human DNA	C 554	17	3.1	135176	75	AC073907	AC073907 Homo sapi
C 482	17	3.1	89453	12	AC068655	AC068655 Genomic s	C 555	17	3.1	135551	2	D90906	D90906 Synchocyst
C 483	17	3.1	90448	12	AC079730	AC079730 Arabidops	C 556	17	3.1	137159	74	AC069090	AC069090 Homo sapi
C 484	17	3.1	90448	12	AC079733	AC079733 Arabidops	C 557	17	3.1	137304	86	AC005627	AC005627 Homo sapi
C 485	17	3.1	90604	86	AC006525	AC006525 Homo sapi	C 558	17	3.1	137557	86	AC005909	AC005909 Homo sapi
C 486	17	3.1	91331	82	AP001970	AP001970 Homo sapi	C 559	17	3.1	137720	85	AC005410	AC005410 Homo sapi
C 487	17	3.1	91549	76	AC079339	AC079339 Homo sapi	C 560	17	3.1	137794	65	AC016854	AC016854 Homo sapi
C 488	17	3.1	93848	80	AL356501	AL356501 Homo sapi	C 561	17	3.1	138490	94	MMJ249895	MMJ249895 Mus muscu
C 489	17	3.1	95096	86	AC008384	AC008384 Homo sapi	C 562	17	3.1	138909	62	AC010612	AC010612 Homo sapi
C 490	17	3.1	95614	63	AC012890	AC012890 Drosophill	C 563	17	3.1	138909	90	CNS01D53	AL121653 BAC seque
C 491	17	3.1	96109	10	AX067460	AX067460 Sequence	C 564	17	3.1	138912	79	AL160257	AL160257 Homo sapi
C 492	17	3.1	96276	92	HS0117516	AL049538 Human DNA	C 565	17	3.1	139301	80	AL359971	AL359971 Homo sapi
C 493	17	3.1	97176	78	AL139249	AL139249 Homo sapi	C 566	17	3.1	139338	83	AP002879	AP002879 Homo sapi
C 494	17	3.1	97454	89	AL139147	AL139147 Human DNA	C 567	17	3.1	139467	6	D90905	D90905 Synchocyst
C 495	17	3.1	98219	85	AC005282	AC005282 Homo sapi	C 568	17	3.1	140000	66	AC019064	AC019064 Homo sapi
C 496	17	3.1	99075	78	AF186996	AF186996 Homo sapi	C 569	17	3.1	140136	89	AL136087	AL136087 Human DNA
C 497	17	3.1	99358	89	AL137858	AL137858 Human DNA	C 570	17	3.1	140357	64	AC016221	AC016221 Homo sapi
C 498	17	3.1	100269	91	HS105C14	AL049610 Human DNA	C 571	17	3.1	140730	90	AP001960	AP001960 Homo sapi
C 499	17	3.1	101615	85	AC004038	AC004038 Homo sapi	C 572	17	3.1	140852	61	AC009734	AC009734 Homo sapi
C 500	17	3.1	106117	82	AP000628	AP000628 Homo sapi	C 573	17	3.1	141103	81	AL445241	AL445241 Homo sapi
C 501	17	3.1	106988	85	AC001226	AC001226 Genomic s	C 574	17	3.1	142055	62	AC010495	AC010495 Homo sapi
C 502	17	3.1	107728	79	AL162721	AL162721 Homo sapi	C 575	17	3.1	142103	81	AL390863	AL390863 Homo sapi
C 503	17	3.1	107728	79	AL162721	AL162721 Homo sapi	C 576	17	3.1	142509	74	AC068571	AC068571 Homo sapi
C 504	17	3.1	108040	73	AC068150	AC068150 Homo sapi	C 577	17	3.1	142908	82	AL1513172	AL1513172 Homo sapi
C 505	17	3.1	109173	86	AC007678	AC007678 Homo sapi	C 578	17	3.1	143892	92	HSJ2680N4	HSJ2680N4 Homo sapi
C 506	17	3.1	109201	85	AC000403	AC000403 Genomic s	C 579	17	3.1	143894	74	AC069002	AC069002 Homo sapi
C 507	17	3.1	109723	78	AF165146	AF165146 Homo sapi	C 580	17	3.1	144013	69	AC025059	AC025059 Homo sapi
C 508	17	3.1	110000	60	AC003656	Continuation (6 of	C 581	17	3.1	144234	83	AP002425	AP002425 Homo sapi
C 509	17	3.1	110000	60	AC003656	Continuation (7 of	C 582	17	3.1	144234	82	AP001570	AP001570 Homo sapi
C 510	17	3.1	110000	60	AC007194	Continuation (2 of	C 583	17	3.1	144348	64	AC016423	AC016423 Homo sapi
C 511	17	3.1	110000	64	AL357125	Continuation (2 of	C 584	17	3.1	144391	73	AC055823	AC055823 Homo sapi
C 512	17	3.1	110000	80	AL357125	Continuation (9 of	C 585	17	3.1	144410	68	AC023992	AC023992 Homo sapi
C 513	17	3.1	110000	81	AL390202	Continuation (2 of	C 586	17	3.1	145231	74	AC068992	AC068992 Homo sapi
C 514	17	3.1	110000	81	CEY48G10	Continuation (2 of	C 587	17	3.1	145239	82	AP000653	AP000653 Homo sapi
C 515	17	3.1	110000	83	CEY54E2	Continuation (2 of	C 588	17	3.1	145485	64	AC016533	AC016533 Homo sapi
C 516	17	3.1	111566	12	AC000348	Continuation (2 of	C 589	17	3.1	145767	62	AC011094	AC011094 Homo sapi
C 517	17	3.1	111566	12	AC000348	Continuation (2 of	C 590	17	3.1	145846	66	AC020298	AC020298 Drosophill
C 518	17	3.1	112632	78	AL137158	AL137158 Homo sapi	C 591	17	3.1	145871	95	AL1391601	AL1391601 Homo sapi
C 519	17	3.1	112632	78	AL137158	AL137158 Homo sapi	C 592	17	3.1	146059	60	AC019030	AC019030 Homo sapi
C 520	17	3.1	112902	85	AC005230	AC005230 Homo sapi	C 593	17	3.1	146077	68	AC023380	AC023380 Homo sapi
C 521	17	3.1	113280	81	AL390236	AL390236 Homo sapi	C 594	17	3.1	146420	80	AL358875	AL358875 Homo sapi
C 522	17	3.1	113826	89	AL133378	AL133378 Human DNA	C 595	17	3.1	146691	83	AP002402	AP002402 Homo sapi

C 596	17	3.1 146831	91	HS523C21	AL021408 Homo sapi	669	17	3.1 160168	91	CNS05TDH	AL356799 Human chr
C 597	17	3.1 147174	13	AP000492	AP000492 Oryza sat	670	17	3.1 160225	72	AC037438	AC037438 Homo sapi
C 598	17	3.1 147240	79	AL353720	AL353720 Homo sapi	671	17	3.1 160436	73	AC067855	AC067855 Homo sapi
C 599	17	3.1 147448	63	AC012272	AC012272 Homo sapi	672	17	3.1 160480	12	AF123535	AF123535 Zea mays
C 600	17	3.1 147712	87	AC011299	AC011299 Homo sapi	673	17	3.1 160559	69	AC025149	AC025149 Homo sapi
C 601	17	3.1 147847	82	AL513213	AL513213 Homo sapi	674	17	3.1 160583	62	NC010968	NC010968 Homo sapi
C 602	17	3.1 148191	80	AL356391	AL356391 Homo sapi	675	17	3.1 161192	66	AC020720	AC020720 Homo sapi
C 603	17	3.1 148400	79	AL354749	AL354749 Homo sapi	676	17	3.1 161346	81	AL391864	AL391864 Homo sapi
C 604	17	3.1 148583	83	CEY11D7	Z92818 Caenorhabdi	677	17	3.1 161596	76	AC079586	AC079586 Homo sapi
C 605	17	3.1 148595	72	AC036129	AC036129 Homo sapi	678	17	3.1 161903	71	AC027206	AC027206 Homo sapi
C 606	17	3.1 149087	89	AL157826	AL157826 Human DNA	679	17	3.1 162002	87	AC022697	AC022697 Homo sapi
C 607	17	3.1 149101	74	AC069375	AC069375 Homo sapi	680	17	3.1 162237	89	AL133549	AL133549 Human DNA
C 608	17	3.1 149124	78	AL136079	AL136079 Homo sapi	681	17	3.1 162354	75	AC073299	AC073299 Homo sapi
C 609	17	3.1 149220	68	AC023539	AC023539 Homo sapi	682	17	3.1 162463	80	AL359760	AL359760 Homo sapi
C 610	17	3.1 149607	67	AC022109	AC022109 Homo sapi	683	17	3.1 162493	74	AC068776	AC068776 Homo sapi
C 611	17	3.1 149919	67	AC022545	AC022545 Homo sapi	684	17	3.1 162590	72	AC036203	AC036203 Homo sapi
C 612	17	3.1 150027	64	AC015596	AC015596 Homo sapi	685	17	3.1 162695	89	AL353580	AL353580 Homo sapi
C 613	17	3.1 150902	68	AC023106	AC023106 Homo sapi	686	17	3.1 162731	74	AC068326	AC068326 Homo sapi
C 614	17	3.1 151073	88	AC073141	AC073141 Homo sapi	687	17	3.1 162764	70	AC026063	AC026063 Homo sapi
C 615	17	3.1 151879	80	AL355813	AL355813 Homo sapi	688	17	3.1 162775	64	AC015896	AC015896 Homo sapi
C 616	17	3.1 152103	63	AC012130	AC012130 Homo sapi	689	17	3.1 162912	92	HSAC002067	HSAC002067
C 617	17	3.1 153141	73	AC062021	AC062021 Homo sapi	690	17	3.1 162968	79	AL354978	AL354978 Homo sapi
C 618	17	3.1 153364	61	AC009787	AC009787 Homo sapi	691	17	3.1 162975	69	AC025225	AC025225 Homo sapi
C 619	17	3.1 153463	69	AC024643	AC024643 Homo sapi	692	17	3.1 162993	82	AP000889	AP000889 Homo sapi
C 620	17	3.1 153946	60	AC008673	AC008673 Homo sapi	693	17	3.1 163268	66	NC019159	NC019159 Homo sapi
C 621	17	3.1 154353	61	AC010472	AC010472 Homo sapi	694	17	3.1 163712	85	AC004065	AC004065 Homo sapi
C 622	17	3.1 154453	62	AC011179	AC011179 Homo sapi	695	17	3.1 163929	71	AC027686	AC027686 Homo sapi
C 623	17	3.1 154561	13	AP002819	AP002819 Oryza sat	696	17	3.1 164112	75	AC073193	AC073193 Homo sapi
C 624	17	3.1 154666	69	AC025182	AC025182 Homo sapi	697	17	3.1 164229	86	AC006386	AC006386 Homo sapi
C 625	17	3.1 154784	69	AC025362	AC025362 Homo sapi	698	17	3.1 164286	77	AC079839	AC079839 Homo sapi
C 626	17	3.1 154796	86	AC007372	AC007372 Homo sapi	699	17	3.1 164309	73	NC067834	NC067834 Homo sapi
C 627	17	3.1 154825	72	NC053517	NC053517 Homo sapi	700	17	3.1 164354	77	AC084811	AC084811 Homo sapi
C 628	17	3.1 154923	78	AL138781	AL138781 Homo sapi	701	17	3.1 164604	74	AC027383	AC027383 Homo sapi
C 629	17	3.1 155146	69	AC025216	AC025216 Homo sapi	702	17	3.1 164719	71	AC068623	AC068623 Homo sapi
C 630	17	3.1 155436	73	AC009666	AC009666 Homo sapi	703	17	3.1 164798	62	AC010651	AC010651 Homo sapi
C 631	17	3.1 155779	61	AC068260	AC068260 Homo sapi	704	17	3.1 164833	69	AC024296	AC024296 Homo sapi
C 632	17	3.1 155868	65	NC018956	NC018956 Homo sapi	705	17	3.1 164924	79	AL354941	AL354941 Homo sapi
C 633	17	3.1 155941	76	NC079211	NC079211 Homo sapi	706	17	3.1 164942	69	AC024656	AC024656 Homo sapi
C 634	17	3.1 156361	70	AC026174	AC026174 Homo sapi	707	17	3.1 165190	81	AL390788	AL390788 Homo sapi
C 635	17	3.1 156378	77	AC084267	AC084267 Homo sapi	708	17	3.1 165711	62	AC011884	AC011884 Homo sapi
C 636	17	3.1 156681	67	AC022418	AC022418 Homo sapi	709	17	3.1 165901	94	MM437P9	MM437P9 Mus muscu
C 637	17	3.1 156776	70	AC026528	AC026528 Homo sapi	710	17	3.1 166197	75	AC073552	AC073552 Homo sapi
C 638	17	3.1 156783	69	AC025482	AC025482 Homo sapi	711	17	3.1 166234	91	HS273P12	HS273P12 Homo sapi
C 639	17	3.1 156838	76	NC078862	NC078862 Homo sapi	712	17	3.1 166272	60	AC007841	AC007841 Homo sapi
C 640	17	3.1 156955	61	AC009419	AC009419 Homo sapi	713	17	3.1 166344	79	AL162577	AL162577 Homo sapi
C 641	17	3.1 157001	90	CNS01DX7	AL139099 Human chr	714	17	3.1 166819	83	CEY22F5	Z99712 Caenorhabdi
C 642	17	3.1 157051	62	AC011095	AC011095 Homo sapi	715	17	3.1 166862	74	AC069533	AC069533 Homo sapi
C 643	17	3.1 157122	77	AC087109	AC087109 Homo sapi	716	17	3.1 166966	78	AL138685	AL138685 Homo sapi
C 644	17	3.1 157348	83	AP002446	AP002446 Homo sapi	717	17	3.1 167025	90	AL445439	AL445439 Homo sapi
C 645	17	3.1 157393	72	NC036212	NC036212 Homo sapi	718	17	3.1 167257	86	AC008008	AC008008 Homo sapi
C 646	17	3.1 157611	72	AC040910	AC040910 Homo sapi	719	17	3.1 167441	75	AC073832	AC073832 Homo sapi
C 647	17	3.1 157613	87	AC018769	AC018769 Homo sapi	720	17	3.1 167494	82	AP002088	AP002088 Homo sapi
C 648	17	3.1 157769	76	AC074193	AC074193 Homo sapi	721	17	3.1 167571	71	AC027761	AC027761 Homo sapi
C 649	17	3.1 157889	77	AC079996	AC079996 Homo sapi	722	17	3.1 167700	86	AC007036	AC007036 Homo sapi
C 650	17	3.1 157903	13	AP000570	AP000570 Oryza sat	723	17	3.1 167721	71	AC030219	AC030219 Homo sapi
C 651	17	3.1 158019	79	AL354774	AL354774 Homo sapi	724	17	3.1 167803	62	AC010816	AC010816 Homo sapi
C 652	17	3.1 158116	80	AL357622	AL357622 Homo sapi	725	17	3.1 167830	66	AC020678	AC020678 Homo sapi
C 653	17	3.1 158207	67	AC021942	AC021942 Homo sapi	726	17	3.1 167830	71	AC027768	AC027768 Homo sapi
C 654	17	3.1 158334	70	AC025858	AC025858 Homo sapi	727	17	3.1 168475	64	AC015698	AC015698 Homo sapi
C 655	17	3.1 158280	62	AC011087	AC011087 Homo sapi	728	17	3.1 167932	73	AC068133	AC068133 Homo sapi
C 656	17	3.1 158483	70	AC025987	AC025987 Homo sapi	729	17	3.1 168079	69	AC024709	AC024709 Homo sapi
C 657	17	3.1 158714	12	NC082644	NC082644 Oryza sat	730	17	3.1 168247	83	AC005014	AC005014 Homo sapi
C 658	17	3.1 158905	86	AC005666	AC005666 Homo sapi	731	17	3.1 168362	85	AC012413	AC012413 Homo sapi
C 659	17	3.1 159487	81	AL441963	AL441963 Homo sapi	732	17	3.1 168475	64	AC015698	AC015698 Homo sapi
C 660	17	3.1 159577	77	AC080060	AC080060 Homo sapi	733	17	3.1 168544	78	AC087564	AC087564 Homo sapi
C 661	17	3.1 159612	74	AC069095	AC069095 Homo sapi	734	17	3.1 168607	90	CNS00000F	AL049837 Human chr
C 662	17	3.1 159725	76	AC079320	AC079320 Homo sapi	735	17	3.1 168903	11	AF158101	AF158101 Bacterioph
C 663	17	3.1 159777	78	AF306443	AF306443 Homo sapi	736	17	3.1 169172	70	AC026663	AC026663 Homo sapi
C 664	17	3.1 159824	79	AL353649	AL353649 Homo sapi	737	17	3.1 169184	90	AL356969	AL356969 Homo sapi
C 665	17	3.1 159857	87	AC018767	AC018767 Homo sapi	738	17	3.1 169299	62	AC011750	AC011750 Homo sapi
C 666	17	3.1 159976	74	AC016124	AC016124 Homo sapi	739	17	3.1 169362	78	AL136440	AL136440 Homo sapi
C 667	17	3.1 160007	64	AC068892	AC068892 Homo sapi	740	17	3.1 169515	68	AC023213	AC023213 Homo sapi
C 668	17	3.1 160112	72	AC046171	AC046171 Homo sapi	741	17	3.1 169516	63	AC013934	AC013934 Drosophila

742	17	3.1	169610	79	AL354854	Homo sapi	C 815	17	3.1	178367	64	AC015614	AC015614 Homo sapi
743	17	3.1	169700	60	AC008437	Homo sapi	C 816	17	3.1	178443	75	AC073348	AC073348 Homo sapi
744	17	3.1	169884	66	AC020596	Homo sapi	C 817	17	3.1	178632	80	AL359998	AL359998 Homo sapi
745	17	3.1	170064	68	AC022771	Homo sapi	C 818	17	3.1	178929	90	AL359252	AL359252 Homo sapi
746	17	3.1	170189	71	AC027615	Homo sapi	C 819	17	3.1	179075	65	AC018518	AC018518 Homo sapi
747	17	3.1	170218	73	AC068125	Homo sapi	C 820	17	3.1	179162	82	AP001823	AP001823 Homo sapi
748	17	3.1	170402	77	AC080097	Homo sapi	C 821	17	3.1	179207	61	AC009920	AC009920 Homo sapi
749	17	3.1	170421	79	AL158191	Homo sapi	C 822	17	3.1	179518	76	AC079203	AC079203 Homo sapi
750	17	3.1	170452	88	AF152364	Homo sapi	C 823	17	3.1	179563	86	AC006433	AC006433 Homo sapi
751	17	3.1	170466	60	AC007997	Homo sapi	C 824	17	3.1	179681	63	AC013785	AC013785 Homo sapi
752	17	3.1	170571	71	AC031984	Homo sapi	C 825	17	3.1	179789	75	AC073349	AC073349 Homo sapi
753	17	3.1	170976	75	AC037981	Homo sapi	C 826	17	3.1	180153	65	AC018798	AC018798 Homo sapi
754	17	3.1	171034	82	AP001325	Homo sapi	C 827	17	3.1	180179	65	AC018881	AC018881 Homo sapi
755	17	3.1	171200	70	AC025801	Homo sapi	C 828	17	3.1	180501	70	AC026789	AC026789 Homo sapi
756	17	3.1	171235	76	AC079444	Mus muscu	C 829	17	3.1	180551	93	HUAC004158	HUAC004158 Homo sapi
757	17	3.1	171426	75	AC074041	Mus muscu	C 830	17	3.1	180791	68	AC023977	AC023977 Homo sapi
758	17	3.1	171462	80	AL358052	Homo sapi	C 831	17	3.1	180827	86	AC007344	AC007344 Homo sapi
759	17	3.1	171505	83	CNS01DTH	Homo sapi	C 832	17	3.1	181116	68	AC023315	AC023315 Homo sapi
760	17	3.1	171894	61	AC009266	Homo sapi	C 833	17	3.1	181121	64	AC016073	AC016073 Homo sapi
761	17	3.1	171992	79	AL160269	Homo sapi	C 834	17	3.1	181166	69	AC025251	AC025251 Homo sapi
762	17	3.1	172200	60	AC007219	Homo sapi	C 835	17	3.1	181254	82	AP000825	AP000825 Homo sapi
763	17	3.1	172591	87	AC022401	Homo sapi	C 836	17	3.1	181406	77	AC079832	AC079832 Homo sapi
764	17	3.1	172738	75	AC074104	Homo sapi	C 837	17	3.1	181671	86	AC007040	AC007040 Homo sapi
765	17	3.1	172879	74	AC068487	Homo sapi	C 838	17	3.1	181772	60	AC007689	AC007689 Homo sapi
766	17	3.1	173019	73	AC060228	Homo sapi	C 839	17	3.1	181827	68	AC022942	AC022942 Homo sapi
767	17	3.1	173091	70	AC026095	Homo sapi	C 840	17	3.1	181956	81	AL391495	AL391495 Homo sapi
768	17	3.1	173175	80	AL359208	Homo sapi	C 841	17	3.1	182018	63	AC012455	AC012455 Homo sapi
769	17	3.1	173467	71	AC027446	Homo sapi	C 842	17	3.1	182150	92	HS6278N14	HS6278N14 Homo sapi
770	17	3.1	173760	89	AL354653	Human DNA	C 843	17	3.1	182189	75	AC073409	AC073409 Homo sapi
771	17	3.1	173838	67	AC021481	Homo sapi	C 844	17	3.1	182372	86	AC006035	AC006035 Homo sapi
772	17	3.1	173874	73	AC067791	Homo sapi	C 845	17	3.1	182467	63	AC012203	AC012203 Homo sapi
773	17	3.1	174019	90	AP001538	Homo sapi	C 846	17	3.1	182625	65	AC018704	AC018704 Homo sapi
774	17	3.1	174069	70	AC026852	Homo sapi	C 847	17	3.1	182703	75	AC073117	AC073117 Homo sapi
775	17	3.1	174114	60	AC007481	Homo sapi	C 848	17	3.1	182800	62	AC011232	AC011232 Homo sapi
776	17	3.1	174280	80	AL356116	Homo sapi	C 849	17	3.1	182905	68	AC022885	AC022885 Homo sapi
777	17	3.1	174473	71	AC027728	Homo sapi	C 850	17	3.1	182959	83	CNS01RRM	CNS01RRM Homo sapi
778	17	3.1	174596	68	AC022812	Homo sapi	C 851	17	3.1	183115	89	AL138916	AL138916 Homo sapi
779	17	3.1	174927	81	AL445427	Homo sapi	C 852	17	3.1	183201	75	AC074006	AC074006 Homo sapi
780	17	3.1	175056	82	AP002368	Homo sapi	C 853	17	3.1	183337	89	AL139002	AL139002 Homo sapi
781	17	3.1	175076	72	AC048365	Homo sapi	C 854	17	3.1	183345	74	AC068519	AC068519 Homo sapi
782	17	3.1	175228	80	AL357053	Homo sapi	C 855	17	3.1	183407	82	AP000868	AP000868 Homo sapi
783	17	3.1	175230	81	AL449343	Homo sapi	C 856	17	3.1	183551	79	AL162254	AL162254 Homo sapi
784	17	3.1	175288	74	AC068780	Homo sapi	C 857	17	3.1	183684	89	AL133330	AL133330 Human DNA
785	17	3.1	175308	87	AC026650	Homo sapi	C 858	17	3.1	183688	64	AC016378	AC016378 Homo sapi
786	17	3.1	175504	70	AC010183	Homo sapi	C 859	17	3.1	183820	79	AL354744	AL354744 Homo sapi
787	17	3.1	175577	67	AC022462	Homo sapi	C 860	17	3.1	184031	81	AL512402	AL512402 Homo sapi
788	17	3.1	175741	66	AC021001	Homo sapi	C 861	17	3.1	184169	70	AC026349	AC026349 Homo sapi
789	17	3.1	175918	65	AC016710	Homo sapi	C 862	17	3.1	184357	60	AC008549	AC008549 Homo sapi
790	17	3.1	175928	73	AC067849	Homo sapi	C 863	17	3.1	184684	79	AL162732	AL162732 Homo sapi
791	17	3.1	175987	83	CNS057C7	Homo sapi	C 864	17	3.1	185043	65	AC018964	AC018964 Homo sapi
792	17	3.1	176033	79	AL161794	Homo sapi	C 865	17	3.1	185076	65	AC018965	AC018965 Homo sapi
793	17	3.1	176204	77	AC084767	Oryza sat	C 866	17	3.1	185078	94	AC026281	AC026281 Homo sapi
794	17	3.1	176422	89	AL354853	Human DNA	C 867	17	3.1	185548	70	AC005743	AC005743 Homo sapi
795	17	3.1	176466	79	AL353783	Homo sapi	C 868	17	3.1	185679	87	AC022534	AC022534 Homo sapi
796	17	3.1	176571	71	AC027111	Homo sapi	C 869	17	3.1	185799	81	AL390238	AL390238 Homo sapi
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798	17	3.1	176818	61	AC009673	Homo sapi	C 871	17	3.1	185977	82	AL513123	AL513123 Homo sapi
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800	17	3.1	176955	83	AP002407	Homo sapi	C 873	17	3.1	186109	83	CNS01BRP0	CNS01BRP0 Homo sapi
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802	17	3.1	177062	61	AC009609	Homo sapi	C 875	17	3.1	186390	68	AC023553	AC023553 Homo sapi
803	17	3.1	177068	82	AP000773	Homo sapi	C 876	17	3.1	186812	63	AC023089	AC023089 Homo sapi
804	17	3.1	177189	83	HS428A13	Homo sapi	C 877	17	3.1	186839	83	CNS01DND	CNS01DND Homo sapi
805	17	3.1	177209	82	AP000424	Homo sapi	C 878	17	3.1	186931	65	AC018861	AC018861 Homo sapi
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C 982	17	3.1	221003	83	CNS01DRW	AL121576 Homo sapi
C 983	17	3.1	221899	76	AC079548	AC079548 Mus muscu
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ALIGNMENTS

RESULT 1	AB010073	80376 bp	DNA	PLN	27-DEC-2000
LOCUS	AB010073	80376 bp	DNA	PLN	27-DEC-2000
DEFINITION	Arabidopsis thaliana genomic DNA, chromosome 5, PI clone:MFBI3.				
ACCESSION	AB010073	BA000015			
VERSION	AB010073.1	GI:2760169			
SOURCE	Arabidopsis thaliana (strain:Columbia) DNA, clone:lib:MFtsul PI clone:MFBI3.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
AUTHORS	1 (sites)				
TITLE	Sato,S., Kaneo,T., Kotani,H., Nakamura,Y., Asamizu,E., MiyaJima,N. and Tabata,S.				
JOURNAL	Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned PI and TAC clones				
MEDLINE	DNA Res. 5 (1), 41-54 (1998)				
REFERENCE	98290546				
AUTHORS	2 (bases 1 to 80376)				
TITLE	Nakamura,Y.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812; Japan (E-mail:ynakamu@kazusa.or.jp, Tel:01-438-52-3935, Fax:01-438-52-3934)				

COMMENT
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd.graph.cgi?c=MFBI3
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
(Informatics Group, Oak Ridge National Laboratory,
http://combio.ornl.gov/Gra11-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://grembl1.zo1.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-se
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-se/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MFBI9 and the 3' clone is MC12.
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IKRELAIPERILYLOENRILIRIPAEICTLONLRHLDVGNHNVGTTIELIRFDS
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misc_feature 8534.8614 /note="similar to EST AA309744 (NID:g1962093)"
misc_feature 8735.8889 /note="similar to EST AA309744 (NID:g1962093)"
repeat_region 8895.8945 /rpt_family="(TG)n"
repeat_region 8991.9013 /rpt_family="(TTG)n"
repeat_region 9038.9121 /rpt_family="MERS3"
misc_feature 9072.9499 /note="similar to EST T91457 (NID:g723370) ye01g08.r1"
misc_feature 9219.9606 /note="match to EST AA533199 (NID:g2277295) n11c11.s1"
repeat_region 9653.9748 /rpt_family="L1"
repeat_region 9999.10295 /rpt_family="L1"
repeat_region 10348.10495 /rpt_family="MIR"
repeat_region 10504.10529 /rpt_family="(TTA)n"
repeat_region 10530.10816 /rpt_family="Alu"
repeat_region 10817.10848 /rpt_family="(TTA)n"
repeat_region 11403.11350 /rpt_family="GA-rich"
misc_feature 12131.12514 /note="match to EST A1637495 (NID:g4689729) tt25f01.x1"
repeat_region 13155.13611 /rpt_family="L1"
repeat_region 13612.13638 /rpt_family="(TAA)n"
repeat_region 13704.13747 /rpt_family="(TG)n"
repeat_region 13849.13932 /rpt_family="MERS3"
repeat_region 14463.14560 /rpt_family="L1"
repeat_region 14779.15099 /rpt_family="L1"
repeat_region 15303.15332 /rpt_family="(TTA)n"
repeat_region 15333.15617 /rpt_family="Alu"
repeat_region 15618.15649
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repeat_region 16200.16292 /rpt_family="GA-rich"
misc_feature 17296.17364 /note="similar to EST AA310709 (NID:g1963058)"
misc_feature 17296.17349 /note="similar to EST C19100 (NID:g1580702)"
repeat_region 17990.18196 /rpt_family="L1"
repeat_region 18197.18499 /rpt_family="Alu"
repeat_region 18500.18621 /rpt_family="L1"
repeat_region 18832.18977 /rpt_family="CT-rich"
repeat_region 18987.19351 /rpt_family="L1"
repeat_region 20180.20500 /rpt_family="MIR"
repeat_region 20587.20757 /rpt_family="Alu"

Query Match 4.08; Score 22; DB 86; Length 133137;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 336 AGTATGTTTCTTATCATTA 357
Db 117618 AGTATGTTTCTTATCATTA 117639

RESULT 3
AC023570 151429 bp DNA HTG 20-SEP-2000
LOCUS Homo sapiens chromosome 7 clone RP11-623K16 map 7, WORKING DRAFT
DEFINITION SEQJENCE, 15 unordered pieces.
ACCESSION AC023570
VERSION AC023570.3 GI:10198523
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT;
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 151429)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 7, clone RP11-623K16
Unpublished
2 (bases 1 to 151429)
REFERENCE 2 (bases 1 to 151429)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bede,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearlall,K., Dewar,K., Dodge,S., Domingo,M., Doyle,M.,
Fenster,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-pierre,N., Grant,G., Hages,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Laroque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,J.,
Meneus,L., Mihova,T., Miranda,C., Mienna,Y., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olyar,T.M.,
Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tittell,A.,
Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.
Direct Submission
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 20, 2000 this sequence version replaced gi:9167819.
```


All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L6780
Center clone name: 623_K16
----- Summary Statistics -----
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144705 bases at least Q40
Consensus quality: 147875 bases at least Q30
Consensus quality: 149247 bases at least Q20
Insert size: 15700; agarose-fp
Insert size: 150029; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 5.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. 8036: contig of 8036 bp in length
1
8037 8136: gap of 100 bp
8137 10849: contig of 2713 bp in length
10850 10949: gap of 100 bp
10950 32703: contig of 21754 bp in length
32704 32803: gap of 100 bp
32804 37751: contig of 4948 bp in length
37752 37851: gap of 100 bp
37852 43829: contig of 5978 bp in length
43830 43929: gap of 100 bp
43930 50340: contig of 6411 bp in length
50341 50440: gap of 100 bp
50441 55479: contig of 5039 bp in length
55480 55579: gap of 100 bp
55580 62760: contig of 7181 bp in length
62761 62860: gap of 100 bp
62861 72470: contig of 9610 bp in length
72471 72570: gap of 100 bp
72571 83146: contig of 10576 bp in length
83147 83246: gap of 100 bp
83247 98629: contig of 15383 bp in length
98630 98729: gap of 100 bp
98730 113955: contig of 15226 bp in length
113956 114055: gap of 100 bp
114056 128189: contig of 14134 bp in length
128190 128289: gap of 100 bp
128290 148106: contig of 19817 bp in length
148107 148206: gap of 100 bp
148207 151429: contig of 3223 bp in length.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-623K16"
/clone_lib="RPCT-11 Human Male BAC"
1. 8036
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
misc_feature
8137. 10849
misc_feature

misc_feature /note="assembly_fragment"
10950. 32703
/note="assembly_fragment"
misc_feature 32804. 37751
/note="assembly_fragment"
misc_feature 37852. 43829
/note="assembly_fragment"
misc_feature 43930. 50340
/note="assembly_fragment"
misc_feature 50441. 55479
/note="assembly_fragment"
misc_feature 55580. 62760
/note="assembly_fragment"
misc_feature 62861. 72470
/note="assembly_fragment"
misc_feature 72571. 83146
/note="assembly_fragment"
misc_feature 83247. 98629
/note="assembly_fragment"
misc_feature 98730. 113955
/note="assembly_fragment"
misc_feature 114056. 128189
/note="assembly_fragment"
misc_feature 128290. 148106
/note="assembly_fragment"
misc_feature 148207. 151429
/note="assembly_fragment"
clone_end:T7
vector_side:right"
BASE COUNT 46908 a 29517 c 28636 g 44907 t 1401 others
ORIGIN

Query Match 4.0%; Score 22; DB 68; Length 151429;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 AGTATGTTTTCATCAATA 357
|||||
Db 93038 AGTATGTTTTCATCAATA 93059

RESULT 4
AC012690/c DNA 21-OCT-2000
LOCUS Homo sapiens chromosome 10 clone RP11-127B19, WORKING DRAFT
DEFINITION AC012690
SEQUENCE, 15 unordered pieces.
ACCESSION AC012690.7 GI:10944434
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 172127)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172127)
AUTHORS Smith,D.R.
TITLE Direct Submission
COMMENT Submitted (03-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Oct 21, 2000 this sequence version replaced gi:6862733.
----- Genome Center
Center: Genome Therapeutics Corporation
Center code: GTC
Web site: <http://www.genomecorp.com/>
Contact: gtc-seqcenter@genomecorp.com
Project Information
Center project name: hg054
----- Summary Statistics -----

Sequencing vector: N/A
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 990315
 Consensus quality: 148903 bases at least Q40
 Consensus quality: 159968 bases at least Q30
 Consensus quality: 162621 bases at least Q20
 Insert size: 170826; sum-of-coverage
 Quality coverage: 4.6x in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1059: contig of 1059 bp in length
 * 1060 1159: gap of unknown length
 * 1160 2591: contig of 1432 bp in length
 * 2592 2691: gap of unknown length
 * 2692 3804: contig of 1113 bp in length
 * 3805 3904: gap of unknown length
 * 3905 5041: contig of 1137 bp in length
 * 5042 5141: gap of unknown length
 * 5142 6813: contig of 1672 bp in length
 * 6814 6913: gap of unknown length
 * 6914 8536: contig of 1623 bp in length
 * 8537 8636: gap of unknown length
 * 8637 10627: contig of 1991 bp in length
 * 10628 10727: gap of unknown length
 * 10728 12325: contig of 1598 bp in length
 * 12326 12425: gap of unknown length
 * 12426 14823: contig of 2398 bp in length
 * 14824 14923: gap of unknown length
 * 14924 23336: contig of 8413 bp in length
 * 23337 23436: gap of unknown length
 * 23437 35598: contig of 12162 bp in length
 * 35599 35698: gap of unknown length
 * 35699 54658: contig of 18960 bp in length
 * 54659 54758: gap of unknown length
 * 54759 90983: contig of 36225 bp in length
 * 90984 91083: gap of unknown length
 * 91084 129108: contig of 38025 bp in length
 * 129109 129208: gap of unknown length
 * 129209 172127: contig of 42919 bp in length.

FEATURES

SOURCE

1. 172127
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-127B19"
 /clone_1lb="RPF-11"
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 /note="assembly_name:Contig11"
 misc_feature 2692..3804
 /note="assembly_name:Contig19"
 misc_feature 3905..5041
 /note="assembly_name:Contig23"
 misc_feature 5142..6813
 /note="assembly_name:Contig27"
 misc_feature 6914..8536
 /note="assembly_name:Contig28"
 misc_feature 8637..10627
 /note="assembly_name:Contig32"
 misc_feature 10728..12325
 /note="assembly_name:Contig33"
 clone_end:T7
 12426..14823
 /note="assembly_name:Contig34"
 misc_feature 14924..23336

misc_feature /note="assembly_name:Contig35"
 23437..35598
 /note="assembly_name:Contig36"
 clone_end:SP6"
 misc_feature 35699..54658
 /note="assembly_name:Contig37"
 54759..90983
 /note="assembly_name:Contig38"
 91084..129108
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 misc_feature 129209..172127
 /note="assembly_name:Contig40"
 BASE COUNT 48733 a 57356 c 37151 g 47466 t 1421 others
 ORIGIN

Query Match 4.0%; Score 22; DB 63; Length 172127;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 TTTCCTAGTCTCAGTATGTTT 345
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 Db 31919 TTTCCTAGTCTCAGTATGTTT 31898

RESULT 5
 HSATP7A06 348 bp DNA PRI 04-APR-1996
 LOCUS Human Menkes disease gene (ATP7A), exon 6.
 DEFINITION
 ACCESSION U27365
 VERSION U27365.1 GI:987236
 KEYWORDS
 SEGMENT
 SOURCE human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 348)
 Dierick,H.A., Ambrosini,L., Spencer,J., Glover,T.W. and Mercer,J.F.
 TITLE Molecular structure of the Menkes disease gene (ATP7A)
 JOURNAL Genomics 28 (3), 462-469 (1995)

MEDLINE
 96039257
 2 (bases 1 to 348)
 REFERENCE
 Dierick,H.A.
 AUTHORS
 Direct Submission
 JOURNAL Submitted (22-MAY-1995) H.A. Dierick, Pediatrics, University of Michigan, 1301 East Catherine, Ann Arbor, MI 49109-0618, USA

FEATURES

SOURCE

1. 348
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="Xq13"
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 /number=6
 130..229
 /gene="ATP7A"
 /note="exon not sequenced completely; this part of sequence from GenBank Accession Number L06133"
 BASE COUNT 114 a 46 c 73 g 115 t
 ORIGIN

Query Match 3.6%; Score 20; DB 92; Length 348;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 GTATTGTTTCTATCAAT 356
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 Db 68 GTATTGTTTCTATCAAT 87

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RESULT      6
HSM06      403 bp      DNA      PRI      14-JUN-2000
LOCUS      HSM06
DEFINITION  Homo sapiens Menkes disease gene, exon 6.
ACCESSION  X82340
VERSION    X82340.1 GI:854155
KEYWORDS   copper-binding protein; Menkes disease; P-type ATPase;
           transmembrane protein.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 403)
AUTHORS   Turner,Z., Vural,B., Tonnesen,T., Chelly,J., Monaco,A.P. and Horn,N.
TITLE     Characterization of the exon structure of the Menkes disease gene
           using vectorette PCR
JOURNAL    Genomics 26 (3), 437-442 (1995)
MEDLINE    95331777
REFERENCE  2 (bases 1 to 403)
AUTHORS   Turner,Z.
TITLE     Direct Submission
COMMENT    Submitted (27-OCT-1994) Z. Turner, John F. Kennedy Inst., 7
           GL Landevej, 2600 Glostrup, DENMARK
REMARK     Revised by author 22-NOV-94
           Related entries: X69208 and L06133.
FEATURES   Location/Qualifiers
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            113..276
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             /number=6
             /usedin=X82336.md_cds
BASE COUNT  141 a      47 c      85 g      128 t      2 others
ORIGIN
Query Match      3.6%; Score 20; DB 92; Length 403;
Best Local Similarity 100.0%; Pred No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 337 GTATGTTTCTTATCAAT 356
Db 85 GTATGTTTCTTATCAAT 104

RESULT      7
CEL04A9
LOCUS      CEL04A9 52946 bp      DNA      INV      14-DEC-1995
DEFINITION  Caenorhabditis elegans cosmid R04A9.
ACCESSION  U41550
VERSION    U41550.1 GI:1118045
KEYWORDS   .
SOURCE     Caenorhabditis elegans strain-Bristol N2.
ORGANISM   Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Pelodetidae; Caenorhabditis.
1 (bases 1 to 52946)
Wilson,R., Alnscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Lalster,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurtry,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Ritken,L., Roopar,A.,
Saunders,D., Showkhen,R., Smaldon,N., Smith,A., Sonhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Wellstock,L.,
Wilkinson-Spoat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

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JOURNAL      Nature 368 (6466), 32-38 (1994)
MEDLINE      94150718
REFERENCE    Geisel,C.
AUTHORS     The sequence of C. elegans cosmid R04A9
TITLE       Unpublished (1995)
JOURNAL      3 (bases 1 to 52946)
AUTHORS     Waterston,R.
TITLE       Direct Submission
COMMENT      Submitted (29-NOV-1995) Robert Waterston
           Submitted by:
           Genome Sequencing Center
           Department of Genetics, Washington University,
           St. Louis, MO 63110, USA, and
           Sanger Centre, Hinxton Hall
           Cambridge CB10 1RQ, England
           e-mail: twenematode.wustl.edu and jesse@sanger.ac.uk
           NEIGHBORING COSMID INFORMATION:
           5' cosmid is C04E7, 200 bp overlap; 3' cosmid is ZK1193, 18200 bp
           overlap. Actual start of this cosmid is at base position 1 of
           CELR04A9; actual end is at 4542 of CELZK1193
NOTES:
Coding sequences below are predicted from computer analysis, using
the program GeneFinder(P. Green and L. Hillier, ms in preparation).
Location/Qualifiers
1..52946
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/map="X"
585..4982
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2827..3155,3203..3396,3721..4126,4173..4524,4581..4771,
4820..4982)
/gene="R04A9.2"
/note="coded for by C. elegans cDNA yk63h11.5; coded for
by C. elegans cDNA yk30g5.5; coded for by C. elegans cDNA
yk30b2.5; coded for by C. elegans cDNA CEES933r; coded for
by C. elegans cDNA yk88d6.5; coded for by C. elegans cDNA
yk37e10.5; coded for by C. elegans cDNA yk30d2.3; coded
for by C. elegans cDNA yk37e10.3; coded for by C. elegans
cDNA yk30g5.3; similar to C. elegans protein C14B1.7"
/codon_start=1
/protein_id="AAA83284.1"
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/translation="MDLIDKVGEGSRPGSTAKKPAATASSTPRTNWTGAKRSSQ
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RPMHDIILKYPERKIGOOTIOISSTPAKRFMDHGGKOTIDIVIRKLMPKCGGTFELI
DPEBSVGRHVCCNNSAEMRAKLYAKTQITGEMSGVARTARDIDKVFDDPPIVGV
AVSLHSAQILGGEYSFOESRLKLTNLOEKMOICINAEQSSSYLPEVVVYRVSGGE
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SCTGVDAVGAISHGEFTICQOTPLIGVTKPKYIYNDCGMSNEEMANTYHILAF
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complement(join(5721..5776,5822..5980,6616..6726,
6771..6840,7591..7759,7800..7906,8726..8812,8855..8899))
/gene="R04A9.3"
/codon_start=1
/evidence="not_experimental"

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gene

CDS

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 PVDGRTIEGSHWVDESILTEGAMPVAKRGSTVIGSINQNSLIGCAHVEADTTIS
 QVAKLVEAOTSAPLQOFADKLSGFVFFVFSATLIVIGLNFLEVEYFER
 GYNREISRETFIRAFQASTIVLCIACCSIGLAPRPMVGTGCGAQNGLIKGCE
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 EHERGRTAVLVAVDGELGLIAIDTVPEAEALAIHLKSGLEVLATGDNSTAR
 STASQOATKVAEVLPSHKVAKVLOEGEKRVAMVGGINDSPALMANANYGIAIGT
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 1708. 2008
 /note="AlusX repeat: matches 302. .1 of consensus"
 2270. .2571
 /note="AlusP repeat: matches 1. .303 of consensus"
 3879. .3958
 repeat_region
 /note="L1ME3 repeat: matches 437. .516 of consensus"
 4211. 4513
 /note="AlusQ repeat: matches 1. .303 of consensus"
 5838. .5863
 /note="L13 copies of 2 mer 100 & conserved"
 6373. .6576
 /note="MER3 repeat: matches 5. .209 of consensus"
 7052. 7243
 repeat_region
 /note="AlusQ repeat: matches 194. .3 of consensus;
 incomplete repeat"
 repeat_region
 /note="MIR2 repeat: matches 17. .142 of consensus"
 7687. .7811
 /note="AlusX repeat: matches 5. .301 of consensus"
 8805. .9101
 /note="AlusX repeat: matches 5. .301 of consensus"
 9389. 9454
 /note="2 copies of 33 mer 91 & conserved"
 10448. .10741
 /note="AlusQ repeat: matches 1. .300 of consensus"
 11141. .11418
 /note="L1MA2 repeat: matches 12. .311 of consensus"
 11765. .11867
 /note="L1MB6 repeat: matches 809. .912 of consensus"
 11806. .11883
 /note="L1MA10 repeat: matches 996. .1069 of consensus"
 12855. .13154
 /note="AlusX repeat: matches 1. .301 of consensus"
 13156. .13328
 /note="MER42B repeat: matches 1025. .1204 of consensus"
 13210. .13350
 /note="MER42C repeat: matches 1183. .1325 of consensus"
 13217. .13407
 /note="L1MC3 repeat: matches 2278. .2452 of consensus"
 13409. .13700
 /note="AlusQ repeat: matches 295. .2 of consensus"
 15220. .15353
 /note="AlusB repeat: matches 14. .142 of consensus;
 incomplete repeat"
 15357. .15655
 /note="AlusQ repeat: matches 1. .299 of consensus"
 15656. .15824
 /note="AlusD repeat: matches 134. .302 of consensus;
 incomplete repeat"
 15982. .16678
 /note="L1 repeat: matches 4904. .4191 of consensus"
 16679. .16978
 /note="AlusQ repeat: matches 299. .1 of consensus"
 16983. .18272
 /note="L1 repeat: matches 2906. .1620 of consensus"
 18298. .18545
 /note="MER25 repeat: matches 1806. .1526 of consensus"
 19460. .20291
 repeat_region

/note="L1 repeat: matches 4546. .5390 of consensus"
 20148. .21015
 /note="L1PA16 repeat: matches 1. .865 of consensus"
 21028. .21327
 /note="AlusX repeat: matches 1. .300 of consensus"
 21350. .21388
 /note="L1PA15 repeat: matches 859. .897 of consensus"
 21413. .21488
 /note="FRAM repeat: matches 158. .83 of consensus"
 22102. .22207
 /note="MIR repeat: matches 174. .63 of consensus"
 22271. .22465
 /note="MIR repeat: matches 262. .56 of consensus"
 23025. .23332
 /note="AlusD repeat: matches 1. .300 of consensus"
 23931. .24072
 /note="MER20 repeat: matches 80. .214 of consensus"
 24086. .24379
 /note="AlusB repeat: matches 5. .302 of consensus"
 24755. .25136
 /note="THE1C repeat: matches 1. .368 of consensus"
 25149. .25313
 /note="THE1B-INTERNAL repeat: matches 1. .164 of consensus"
 25321. .25622
 /note="AlusP repeat: matches 303. .1 of consensus"
 25623. .25768
 /note="THE1B-INTERNAL repeat: matches 150. .295 of
 consensus"
 25770. .26070
 /note="Alus repeat: matches 1. .301 of consensus"
 26086. .26238
 /note="THE1B-INTERNAL repeat: matches 279. .430 of
 consensus"
 26277. .27437
 /note="THE1B-INTERNAL repeat: matches 427. .1580 of
 consensus"
 27438. .27794
 /note="THE1C repeat: matches 1. .369 of consensus"
 29421. .29719
 /note="AlusQ repeat: matches 300. .1 of consensus"
 29759. .29947
 /note="L1MB4 repeat: matches 12. .208 of consensus"
 31239. .31365
 /note="FLAM_A repeat: matches 133. .5 of consensus"
 31720. .31901
 /note="AlusD repeat: matches 121. .300 of consensus;
 incomplete repeat"
 32967. .33267
 /note="AlusQ repeat: matches 1. .300 of consensus"
 33493. .33710
 /note="MIR repeat: matches 9. .248 of consensus"
 33938. .34168
 /note="AlusD repeat: matches 229. .2 of consensus;
 incomplete repeat"
 34810. .35060
 /note="AlusX repeat: matches 300. .55 of consensus;
 incomplete repeat"
 35798. .36059
 /note="L1MA2 repeat: matches 788. .1051 of consensus"
 repeat_region
 Query Match 3.6%; Score 20; DB 91; Length 74432;
 Best local Similarity 100.0%; Pred. NO. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 337 GATTGTTTCTTATCAAT 356
 |||
 Db 40800 GATTGTTTCTTATCAAT 40781
 RESULT 9
 AP001089/c AP001089 87022 bp DNA HTG 30-MAY-2000
 LOCUS Homo sapiens chromosome 18 clone RP11-653M17 map 18p11.3, WORKING
 DEFINITION


```

OY      328      CTAGTCTCAGTATGTTT 347
|||||
Db      27343      CTAGTCTCAGTATGTTT 27324

RESULT 10
AC006778      132749 bp      DNA      HTG      25-FEB-1999
AC006778      Locus
AC006778      DEFINITION
Caenorhabditis elegans clone Y47C4, *** SEQUENCING IN PROGRESS ***
4 unordered pieces.
AC006778      AC006778.3      GI:4309794
HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 132749)
Waterson,R.H.
The sequence of Caenorhabditis elegans clone
Unpublished
2 (bases 1 to 132749)
Waterson,R.H.
Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis
MO 63108, USA
On Mar 1, 1999 this sequence version replaced gi:4263427.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
2080: contig of 2080 bp in length
2081
2095: gap of unknown length
2096: contig of 2148 bp in length
4243
4256: gap of unknown length
4257
13398: contig of 9142 bp in length
13399
13412: gap of unknown length
13413
132749: contig of 119337 bp in length.
Location/Qualifiers
1..132749
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y47C4"

BASE COUNT      42651 a      22976 c      23008 g      44072 t      42 others

ORIGIN
Query Match      3.6%: Score 20; DB 60; Length 132749;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      338      TATTGTTTTCTTATCAATA 357
|||||
Db      128941      TATTGTTTTCTTATCAATA 128960

RESULT 11
AC036162      142362 bp      DNA      HTG      14-MAY-2000
AC036162      Locus
AC036162      DEFINITION
Homo sapiens chromosome 17 clone RP11-143J12 map 17, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
AC036162      AC036162.2      GI:7801461
HTG: HTGS_PHASE1; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
TITLE
1 (bases 1 to 142362)
JOURNAL
Homo sapiens chromosome 17, clone RP11-143u12
AUTHORS
Unpublished
2 (bases 1 to 142362)
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campoliano, A., Castelle, A., Choedel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karlas, A.,
Klein, J., Lacroque, K., Lamazates, R., Landers, T., Lehoczy, J.,
Lewine, R., Lien, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R.,
Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivier, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotلمان, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teisfeyer, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
TITLE
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
JOURNAL
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT
On May 14, 2000 this sequence version replaced gi:7523830.

 COMMENT
 Submitted 07-APR-2000 Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 14, 2000 this sequence version replaced by:7523830.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

 Genomes Project

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- project information -----

```

Center project name: L9139
Center clone name: 143.J.12
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 129334 bases at least Q40
Consensus quality: 136360 bases at least Q30
Consensus quality: 138873 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 140262; sum-of-ctrls
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-ctrls

```

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*-----*
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

*	1	1203:	contlg of 1203 bp	in length
*	1204	1303:	gap of 100 bp	
*	1304	2675:	contlg of 1372 bp	in length
*	2676	2775:	gap of 100 bp	
*	2776	4179:	contlg of 1404 bp	in length
*	4180	4279:	gap of 100 bp	
*	4280	6165:	contlg of 1886 bp	in length
*	6166	6265:	gap of 100 bp	
*	6266	8694:	contlg of 2429 bp	in length
*	8695	8794:	gap of 100 bp	
*	8795	12147:	contlg of 3353 bp	in length

```

* 12148 12247: gap of 100 bp
* 12248 14867: contig of 2620 bp in length
* 14868 14967: gap of 100 bp
* 14968 17734: contig of 2767 bp in length
* 17735 17834: gap of 100 bp
* 17835 20713: contig of 2879 bp in length
* 20714 20813: gap of 100 bp
* 20814 23880: contig of 3067 bp in length
* 23881 23980: gap of 100 bp
* 23981 27122: contig of 3142 bp in length
* 27123 27222: gap of 100 bp
* 27223 30554: contig of 3332 bp in length
* 30555 30654: gap of 100 bp
* 30655 33603: contig of 2949 bp in length
* 33604 33703: gap of 100 bp
* 33704 38236: contig of 4533 bp in length
* 38237 38336: gap of 100 bp
* 38337 43066: contig of 4730 bp in length
* 43067 43166: gap of 100 bp
* 43167 46091: contig of 2925 bp in length
* 46092 46191: gap of 100 bp
* 46192 52025: contig of 5834 bp in length
* 52026 52125: gap of 100 bp
* 52126 60172: contig of 8047 bp in length
* 60173 60272: gap of 100 bp
* 60273 69449: contig of 9177 bp in length
* 69450 69549: gap of 100 bp
* 69550 87646: contig of 18097 bp in length
* 87647 87746: gap of 100 bp
* 87747 112836: contig of 25090 bp in length
* 112837 112936: gap of 100 bp
* 112937 142362: contig of 29426 bp in length.
location/Qualifiers
  1. 142362
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="17"
  /map="17"
  /clone="RP11-143J12"
  /clone_1b="RPC1-11 Human Male BAC"
  1. 1203
  /note="assembly_fragment"
  1304. 2675
  /note="assembly_fragment"
  2776. 4179
  /note="assembly_fragment"
  4280. 6165
  /note="assembly_fragment"
  6266. 8694
  /note="assembly_fragment"
  8795. 12147
  /note="assembly_fragment"
  12248. 14867
  /note="assembly_fragment"
  14968. 17734
  /note="assembly_fragment"
  17835. 20713
  /note="assembly_fragment"
  20814. 23880
  /note="assembly_fragment"
  23981. 27122
  /note="assembly_fragment"
  27223. 30554
  /note="assembly_fragment"
  30655. 33603
  /note="assembly_fragment"
  33704. 38236
  /note="assembly_fragment"
  38337. 43066
  /note="assembly_fragment"
  43167. 46091
  /note="assembly_fragment"
  clone_end:SP6

```

```

misc_feature      vector_side:right"
                  46192..52025
                  /note="assembly_fragment"
misc_feature      52126..60172
                  /note="assembly_fragment"
misc_feature      60273..69449
                  /note="assembly_fragment"
misc_feature      69550..87646
                  /note="assembly_fragment"
misc_feature      87747..112836
                  /note="assembly_fragment"
                  clone_end:T7
misc_feature      vector_side:left"
                  112937..142362
                  /note="assembly_fragment"
BASE COUNT      40507 a 29503 c 29765 g 40480 t 2107 others
ORIGIN

```

```

Query Match      3.6%; Score 20; DB 72; Length 142362;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 328 CTAGTCACGATATGTTT 347
      |||
Db 126690 CTAGTCACGATATGTTT 126709

```

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RESULT 12
AC021110/c      DNA      07-JUL-2000
LOCUS           Homo sapiens chromosome 18 clone RP11-238P13, WORKING DRAFT
DEFINITION      AC021110.3 GI:8439978
ACCESSION       AC021110
VERSION         AC021110
KEYWORDS        HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       1 (bases 1 to 155172)
AUTHORS        Waterston,R.H.
JOURNAL         Unpublished
REFERENCE       2 (bases 1 to 155172)
AUTHORS        Waterston,R.H.
JOURNAL         Direct Submission
                Submitted (14-JAN-2000) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
COMMENT         On Jun 10, 2000 this sequence version replaced g1:7021026.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0238P13
----- Summary Statistics -----
Sequencing vector: M13; 73%
Sequencing vector: plasmid; 27%
Chemistry: Dye-primer ET; 73% of reads
Chemistry: Dye-terminator Big Dye; 27% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 151162 bases at least Q40
Consensus quality: 152443 bases at least Q30
Consensus quality: 153249 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 154672; sum-of-contigs
Quality coverage: 4.08 in Q20 bases; agarose-fp
Quality coverage: 4.69 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently

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* consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 9265: contig of 9265 bp in length
 * 9266 gap of unknown length
 * 9366 contig of 17139 bp in length
 * 26504 gap of unknown length
 * 26505 contig of 17696 bp in length
 * 44301 gap of unknown length
 * 44401 contig of 17850 bp in length
 * 62251 gap of unknown length
 * 62351 contig of 43394 bp in length
 * 105745 gap of unknown length
 * 105845 155172: contig of 49328 bp in length.

FEATURES
 source
 1. .155172
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="18"
 /clone="RP11-238p13"
 1. .9265
 /note="assembly_name:Contig1"
 misc_feature 9366. .26504
 /note="assembly_name:Contig2"
 misc_feature 26505. .44300
 /note="assembly_name:Contig3"
 clone_end:17
 vector_side:right"
 44401. .62250
 /note="assembly_name:Contig4"
 misc_feature 62351. .105744
 /note="assembly_name:Contig5"
 misc_feature 105845. .155172
 /note="assembly_name:Contig6"
 BASE COUNT 51543 a 28385 c 28043 g 46698 t 503 others
 ORIGIN

Query Match 3.6%; Score 20; DB 66; Length 155172;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TAGTGTGTTAAGAACTT 228
 ||||||||||||||||||
 Db 35799 TACTGTGTTAAGAACTT 35780

RESULT 13
 AC011921
 LOCUS Homo sapiens chromosome 17 clone RP11-15E18 map 17, WORKING DRAFT
 DEFINITION
 AC011921
 AC011921.5 GI:12043897
 VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 155261)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 17, clone RP11-15E18
 2 (bases 1 to 155261)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Barina,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Ferreira,P., Fitzhugh,W., Forrest,C., Funke,K., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karats,A., Klein,J.,
 Lehoczy,J., Lien,C., Locke,K., MacDonald,P., Marquis,N.,
 McKean,P., McGurk,A., McKernan,K., McLaughlin,J., Melgrim,J.,
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (16-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 7, 2001 this sequence version replaced gi:9369474.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L3450
 Center clone name: 15_E_18
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 35% of reads
 Sequencing vector: Plasmid; n/a; 65% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.96071
 Consensus quality: 152128 bases at least Q40
 Consensus quality: 152881 bases at least Q30
 Consensus quality: 153204 bases at least Q20
 Insert size: 153000; agarose-fp
 Insert size: 154561; sum-of-contigs
 Quality coverage: 13.7 in Q20 bases; agarose-fp
 Quality coverage: 13.5 in Q20.

NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 64950: contig of 64950 bp in length
 * 64951 gap of 100 bp
 * 65051 66096: contig of 1046 bp in length
 * 66097 66196: gap of 100 bp
 * 66197 68004: contig of 1808 bp in length
 * 68005 68104: gap of 100 bp
 * 68105 72490: contig of 4386 bp in length
 * 72491 72590: gap of 100 bp
 * 72591 91407: contig of 18817 bp in length
 * 91408 91507: gap of 100 bp
 * 91508 109552: contig of 18045 bp in length
 * 109553 109652: gap of 100 bp
 * 109653 147065: contig of 37413 bp in length
 * 147066 147165: gap of 100 bp
 * 147166 155261: contig of 8096 bp in length.

FEATURES
 source
 1. .155261
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="17"
 /map="17"
 /clone="RP11-15E18"
 /clone_lib="RP11 Human Male BAC"
 1. .64950
 /note="assembly_fragment"
 clone_end:sp6
 vector_side:left"
 misc_feature 65051. .66096
 /note="assembly_fragment"


```

http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8265
Center clone name: 634_F_5
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151926 bases at least Q40
Consensus quality: 158244 bases at least Q30
Consensus quality: 160555 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 16194; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently
consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1927: contig of 1927 bp in length
1928 2027: gap of 100 bp
2028 4573: contig of 2546 bp in length
4574 4673: gap of 100 bp
4674 6641: contig of 1968 bp in length
6642 6741: gap of 100 bp
6742 8270: contig of 1529 bp in length
8271 8370: gap of 100 bp
8371 10546: contig of 2176 bp in length
10547 10646: gap of 100 bp
10647 13015: contig of 2369 bp in length
13016 13115: gap of 100 bp
13116 15951: contig of 2836 bp in length
15952 16051: gap of 100 bp
16052 18513: contig of 2462 bp in length
18514 18613: gap of 100 bp
18614 20830: contig of 2217 bp in length
20831 20930: gap of 100 bp
20931 22269: contig of 1339 bp in length
22270 22369: gap of 100 bp
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74237 74336: gap of 100 bp

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	*	91010	101376:	contig of 10276 bp in length
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	*	101477	116514:	contig of 15038 bp in length
	*	116515	116614:	gap of 100 bp
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Job time: 6831 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 01:02:39 ; Search time 115.37 Seconds
(without alignments)
2808.344 Million cell updates/sec

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Gapop 60.0 , Gapept 60.0

Searched: 678276 seqs, 291890651 residues

Word size : 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	3.8	31	18	T79300 Staphylothermus ma
3	21	3.8	52	18	T79299 Staphylothermus ma
4	18	3.2	25002	19	V52181 Streptococcus pneu
5	18	3.2	29604	18	X83005 Human secreted pro
6	17	3.1	157	20	X52014 Human secreted exp
7	17	3.1	209	21	A41434 Human secreted pro
8	17	3.1	361	21	C03852 Human secreted pro
9	17	3.1	432	16	T26471 Human gene signatu
10	17	3.1	486	21	C35823 Zea mays DNA fragm
11	17	3.1	498	21	C94715 Cat flea hindgut a

C 12	17	3.1	849	20	Z16638 Human gene express
C 13	17	3.1	909	21	C74317 Human secreted pro
C 14	17	3.1	1121	11	O06623 Asparagine synthet
C 15	17	3.1	1563	21	A99072 Arabidopsis thalia
C 16	17	3.1	1660	18	T94661 Chrysanthemum flav
C 17	17	3.1	1829	20	X84982 Human secreted pro
C 18	16	2.9	191	16	T21422 Human gene signatu
C 19	16	2.9	269	21	C31195 Human secreted pro
C 20	16	2.9	323	20	X05168 Human MSH5 (hMSH5)
C 21	16	2.9	333	21	A43208 Xenopus secreted e
C 22	16	2.9	482	21	C38143 Zea mays DNA fragm
C 23	16	2.9	500	21	C94177 Cat flea head and
C 24	16	2.9	542	18	T80087 Fragment #2 of the
C 25	16	2.9	593	21	A16400 Human colon cancer
C 26	16	2.9	715	20	Z15052 Human gene express
C 27	16	2.9	830	21	C59909 Human secreted pro
C 28	16	2.9	837	21	A38000 Human secreted pro
C 29	16	2.9	988	21	A02629 Human colon cancer
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C 31	16	2.9	1120	20	X13658 Human secreted pro
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C 33	16	2.9	1221	21	Z33340 Human secreted pro
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C 68	16	2.9	8278	22	C89138 Canine retrovirus
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C 80	16	2.9	1664976	19	V21209 Methanococcus jan
C 81	15	2.7	122	16	T05586 Human islet p69 cd
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C 87	15	2.7	237	21	A65871	E. coli proliferat	C 160	15	2.7	1633	21	C93386	Human secreted pro
C 88	15	2.7	243	21	A41556	Human secreted exp	C 161	15	2.7	1640	12	O10990	Partial sequence o
C 89	15	2.7	244	21	C09203	Human secreted pro	C 162	15	2.7	1641	14	O49931	TNF-R cDNA. Homo
C 90	15	2.7	257	20	X34844	Differentially exp	C 163	15	2.7	1641	15	O45224	Sequence encoding
C 91	15	2.7	261	21	A65991	E. coli proliferat	C 164	15	2.7	1647	21	A40746	Wild type human CD
C 92	15	2.7	269	21	A40748	Wild type human CD	C 165	15	2.7	1656	20	X22125	Human secreted pro
C 93	15	2.7	276	20	V89047	EST clone BV93. H	C 166	15	2.7	1660	19	V48147	Nicotianamine amin
C 94	15	2.7	295	21	C28640	Human secreted pro	C 167	15	2.7	1704	21	C45181	Arabidopsis thalia
C 95	15	2.7	300	20	Z14193	Human gene express	C 168	15	2.7	1720	21	Z96355	S. pneumoniae derl
C 96	15	2.7	313	18	V78666	Staphylococcus aur	C 169	15	2.7	1813	19	V69701	Eucalyptus grandis
C 97	15	2.7	331	21	C06504	Human secreted pro	C 170	15	2.7	1818	11	O03599	Human liver cytoch
C 98	15	2.7	348	21	F21039	Human secreted pro	C 171	15	2.7	1820	21	A40755	Human cytochrome P
C 99	15	2.7	348	21	A34917	Human low adenosin	C 172	15	2.7	1823	20	Z33602	Wild type human CD
C 100	15	2.7	353	21	C09227	Human adenosine re	C 173	15	2.7	1845	20	X19925	Human breast tumou
C 101	15	2.7	377	21	C53208	Human secreted pro	C 174	15	2.7	1852	17	T11381	Mammalian cytochro
C 102	15	2.7	388	21	C03515	Arabidopsis thalia	C 175	15	2.7	1852	17	V44157	Cytochrome P450 2C
C 103	15	2.7	429	21	A79675	Human secreted pro	C 176	15	2.7	1854	17	T11378	Human cytochrome P
C 104	15	2.7	472	18	V75044	Eucalyptus grandis	C 177	15	2.7	1854	19	V44154	Cytochrome P450 2C
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C 106	15	2.7	486	19	T98788	Human secreted pro	C 179	15	2.7	1870	13	O21177	Human CD36 antigen
C 107	15	2.7	495	20	X61626	DNA encoding two S	C 180	15	2.7	1870	17	T14716	Human CD36 antigen
C 108	15	2.7	546	20	X61625	B. burgdorferi ant	C 181	15	2.7	1870	19	V63455	Human putative CD3
C 109	15	2.7	567	20	X13601	B. burgdorferi ant	C 182	15	2.7	1870	21	A50591	Human CD36 antigen
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C 111	15	2.7	631	21	X20952	Arabidopsis thalia	C 184	15	2.7	1884	19	X14587	Wild type human CD
C 112	15	2.7	671	21	F13337	Polynucleotide seq	C 185	15	2.7	1910	21	C77329	H. pylori GHP0 169
C 113	15	2.7	685	20	Z42095	Aspergillus oryzae	C 186	15	2.7	1937	21	A47445	Human ORFX ORF2884
C 114	15	2.7	687	20	X13549	Human endometrium	C 187	15	2.7	1938	21	A47445	Macaque TANGO 232
C 115	15	2.7	716	12	O10059	Enterococcus faeca	C 188	15	2.7	1938	21	C48345	Arabidopsis thalia
C 116	15	2.7	717	12	O10059	Ovine FSH alpha su	C 189	15	2.7	1942	21	A40753	Wild type human CD
C 117	15	2.7	771	21	C76339	Human ORFX ORF1894	C 190	15	2.7	1948	21	C37986	Arabidopsis thalia
C 118	15	2.7	800	20	Z20370	Plant viral move	C 191	15	2.7	1953	20	X55621	Sequence of mouse
C 119	15	2.7	821	21	X13673	Gene encoding bact	C 192	15	2.7	2004	20	X55616	Sequence of mouse
C 120	15	2.7	821	21	C98850	Enterococcus faeca	C 193	15	2.7	2022	21	C44132	zeta mays DNA fragm
C 121	15	2.7	901	21	X55619	Human pancreatic c	C 194	15	2.7	2058	21	C98184	Human colon cancer
C 122	15	2.7	901	21	C46900	Sequence of mouse	C 195	15	2.7	2092	20	X84370	Drosophila Acp76A
C 123	15	2.7	903	21	C43172	Arabidopsis thalia	C 196	15	2.7	2119	21	A09302	Human NIK1 protein
C 124	15	2.7	965	20	X13459	Arabidopsis thalia	C 197	15	2.7	2188	21	F16163	Human prostate can
C 125	15	2.7	977	21	C36434	Enterococcus faeca	C 198	15	2.7	2198	21	A97937	Mung bean alpha 1,
C 126	15	2.7	1011	20	Z41348	Arabidopsis thalia	C 199	15	2.7	2214	21	A26448	Human secreted pro
C 127	15	2.7	1016	17	T48041	Human normal uteru	C 200	15	2.7	2216	21	A40752	Wild type human CD
C 128	15	2.7	1065	21	Z60356	Yeast chromosome I	C 201	15	2.7	2224	16	O89544	p15 Tumour Necrosi
C 129	15	2.7	1086	21	C46471	DNA encoding a 36	C 202	15	2.7	2227	21	A26365	Sequence of mouse
C 130	15	2.7	1184	21	C46473	Arabidopsis thalia	C 203	15	2.7	2251	20	X55608	Human secreted pro
C 131	15	2.7	1192	21	F22356	Human secreted pro	C 204	15	2.7	2251	20	X55609	Mouse clone 65 pro
C 132	15	2.7	1200	21	F16053	Human prostate can	C 205	15	2.7	2265	20	X26288	Human RPL1 8392 ce
C 133	15	2.7	1203	20	Z08866	Mouse interleukin	C 206	15	2.7	2339	12	O10956	Encodes human 75kD
C 134	15	2.7	1203	20	X17787	Mouse interleukin	C 207	15	2.7	2339	20	Z09171	Human tumour necro
C 135	15	2.7	1203	21	A52578	Murine interleukin	C 208	15	2.7	2365	18	V74406	Human cytochrome P
C 136	15	2.7	1216	16	O87295	Rat regucalcin cDN	C 209	15	2.7	2367	20	Z41496	Staphylococcus aur
C 137	15	2.7	1216	21	F13529	Aspergillus oryzae	C 210	15	2.7	2393	12	O10907	Human endometrium
C 138	15	2.7	1290	21	C42067	Arabidopsis thalia	C 211	15	2.7	2394	22	C83951	40kD TNF inhibitor
C 139	15	2.7	1306	13	O27827	Bovine TP (CDNA cl	C 212	15	2.7	2402	20	X26119	Human 40 kDa TNF 1
C 140	15	2.7	1338	20	X61518	B. burgdorferi ant	C 213	15	2.7	2417	21	F16127	DNA sequence of FP
C 141	15	2.7	1341	13	O27559	B. burgdorferi ant	C 214	15	2.7	2478	20	X80148	Human prostate can
C 142	15	2.7	1353	21	Z39862	Human para-influen	C 215	15	2.7	2478	18	V74418	Clostridium histol
C 143	15	2.7	1363	20	X55620	Plasmodium ovale P	C 216	15	2.7	2511	21	F21040	Staphylococcus aur
C 144	15	2.7	1374	15	O72874	Sequence of mouse	C 217	15	2.7	2511	21	A34918	Human low adenosin
C 145	15	2.7	1405	19	V59550	Phosphatase Dbpa.	C 218	15	2.7	2536	21	Z87186	Human adenosine re
C 146	15	2.7	1410	20	X61517	Human secreted pro	C 219	15	2.7	2561	21	A40727	Human Brn1lac cDN
C 147	15	2.7	1419	20	X22716	B. burgdorferi ant	C 220	15	2.7	2561	21	A40745	Wild type human CD
C 148	15	2.7	1473	16	O87715	Human cytochrome P	C 221	15	2.7	2569	21	C93383	Human secreted pro
C 149	15	2.7	1473	17	T28381	Human cytochrome P	C 222	15	2.7	2684	20	Z10170	Human secreted pro
C 150	15	2.7	1473	17	T17404	Human derived cyto	C 223	15	2.7	2745	19	V66367	cDNA encoding a hu
C 151	15	2.7	1475	21	C36317	Arabidopsis thalia	C 224	15	2.7	2792	22	F32738	Human cardiac and
C 152	15	2.7	1477	21	C48471	Arabidopsis thalia	C 225	15	2.7	2794	21	C93393	Human secreted pro
C 153	15	2.7	1490	21	C35129	Arabidopsis thalia	C 226	15	2.7	2828	12	O15171	Human secreted pro
C 154	15	2.7	1504	20	X26116	Fowlpox virus (FPV	C 227	15	2.7	2829	21	Z93333	Bacillus thuringie
C 155	15	2.7	1513	21	C77186	Human ORFX ORF2741	C 228	15	2.7	2853	22	F33096	Partial sequence o
C 156	15	2.7	1521	21	C42268	Arabidopsis thalia	C 229	15	2.7	3017	17	T36776	Human secreted pro
C 157	15	2.7	1562	21	C42467	Arabidopsis thalia	C 230	15	2.7	3017	17	T36786	Prostate-specific

C 231	15	2.7	3104	19	V68343	Transcriptional re
C 232	15	2.7	3106	20	X40172	WO9904265 Seq ID N
C 233	15	2.7	3198	21	F21093	Human low adenosin
C 234	15	2.7	3198	21	A34971	Human adenosine re
C 235	15	2.7	3226	21	A77665	Human PRO1154 cDNA
C 236	15	2.7	3326	21	Z65082	Membrane-bound pro
C 237	15	2.7	3417	21	A70161	Plasmodium falcipar
C 238	15	2.7	3432	20	X20281	Borrelia burgdorfer
C 239	15	2.7	3509	12	Q12287	Metallothionein-11
C 240	15	2.7	3567	18	T47559	42K promoted cytom
C 241	15	2.7	3567	21	A79309	42K promoted cytom
C 242	15	2.7	3657	19	V14015	Pinus radiata cell
C 243	15	2.7	3983	10	N90569	Xenopus paraxial p
C 244	15	2.7	4075	18	T47557	Ovine Y-chromosome
C 245	15	2.7	4075	20	X55618	42K promoted cytom
C 246	15	2.7	4909	18	T47558	Sequence of mouse
C 247	15	2.7	4909	22	F24165	42K promoted cytom
C 248	15	2.7	5727	18	V74501	Human secreted pro
C 249	15	2.7	6252	18	V74361	Staphylococcus aur
C 250	15	2.7	6560	20	X26118	Staphylococcus aur
C 251	15	2.7	6561	20	X26117	DNA sequence of PP
C 252	15	2.7	6645	20	X13432	DNA sequence of PP
C 253	15	2.7	6749	18	T47564	Enterococcus faeca
C 254	15	2.7	6749	18	T47561	Cytomegalovirus pp
C 255	15	2.7	7143	21	A70250	Cytomegalovirus pp
C 256	15	2.7	7722	21	A70168	Plasmodium falcipa
C 257	15	2.7	14078	18	V74502	Staphylococcus aur
C 258	15	2.7	15692	20	X24731	Staphylococcus aur
C 259	15	2.7	15692	20	X24732	London-FAD APP tar
C 260	15	2.7	15701	20	X24733	Swedish-FAD APP713
C 261	15	2.7	16357	21	Z89337	Human UCP3 protein
C 262	15	2.7	16484	20	X13095	Enterococcus faeca
C 263	15	2.7	16595	21	F21095	Human low adenosin
C 264	15	2.7	16595	21	A34973	Human adenosine re
C 265	15	2.7	18436	19	V52220	Streptococcus pneu
C 266	15	2.7	21636	21	A55966	Human G713 3'-end
C 267	15	2.7	28720	19	V49655	Human SC3 DNA. Ho
C 268	15	2.7	32768	20	X12954	Enterococcus faeca
C 269	15	2.7	40138	20	V81946	V. marinus PKS-11k
C 270	15	2.7	40138	21	A71520	MAGE-B cluster DNA
C 271	15	2.7	40352	19	V02032	Polyomphic repeat
C 272	15	2.7	50000	21	A96366	Pg1 genomic coding
C 273	15	2.7	56516	20	Z00870	Wild type PGI codi
C 274	15	2.7	56520	20	X01022	WFS1 variant genom
C 275	15	2.7	67212	21	A08954	BAC containing rep
C 276	15	2.7	83390	21	F22283	BAC containing rep
C 277	15	2.7	90336	21	F22289	Borrelia burgdorfe
C 278	15	2.7	111309	20	X20250	Human kinesin-like
C 279	15	2.7	121162	21	C66548	Olfactory receptor
C 280	15	2.7	144460	21	Z93815	Arabidopsis thalia
C 281	15	2.7	163319	21	F22306	Arabidopsis thalia
C 282	15	2.7	163319	21	F22306	Hereditary haemoch
C 283	15	2.7	235033	19	V57926	Hereditary haemoch
C 284	15	2.7	235033	19	V57926	Hereditary haemoch
C 285	15	2.7	237326	19	V57903	Hereditary haemoch
C 286	15	2.7	237326	19	V57903	Hereditary haemoch
C 287	15	2.7	1038602	20	Z01425	Complete genome se
C 288	15	2.7	1082138	21	F22305	Arabidopsis thalia
C 289	15	2.7	1664976	19	V21209	Methanococcus jann
C 290	15	2.7	1830121	17	T42063	Haemophilus influe
C 291	15	2.5	18	15	Q55292	Cry j 1 cDNA PCR a
C 292	14	2.5	18	18	T80795	Staphylococcus aur
C 293	14	2.5	21	20	Z21760	Exemplary oligonuc
C 294	14	2.5	22	21	A55981	Human G713 PCR pri
C 295	14	2.5	22	14	O52555	HBV target sequenc
C 296	14	2.5	24	19	V19293	H. inselens celluli
C 297	14	2.5	24	21	Z35203	Olestin 16 kDa pro
C 298	14	2.5	25	13	Q34369	Upstream PCR prime
C 299	14	2.5	34	17	V32683	DEAD-box gene PCR
C 300	14	2.5	38	17	T10486	Human wild-type p5
C 301	14	2.5	38	18	T88442	5' PCR primer 3 (s
C 302	14	2.5	41	20	X89736	ClO502 Synthetic O
C 303	14	2.5	54	13	Q33976	Sequence upstream
C 304	14	2.5	55	16	Q74095	Human SDF-1-alpha
C 305	14	2.5	66	18	T69955	Entomopox 42K prom
C 306	14	2.5	71	18	V77639	Staphylococcus aur
C 307	14	2.5	72	22	C87459	Sendai virus PCR p
C 308	14	2.5	72	22	C87460	Sendai virus PCR p
C 309	14	2.5	72	22	C87511	Sendai virus PCR p
C 310	14	2.5	72	22	C87512	Sendai virus PCR p
C 311	14	2.5	92	18	T69951	FlvY matrix (M) ge
C 312	14	2.5	95	13	Q35796	42 KD promoter/F g
C 313	14	2.5	99	18	T47624	42 KD promoter/F g
C 314	14	2.5	104	14	Q37812	Sequence of an alt
C 315	14	2.5	104	19	V42680	Alternative exon f
C 316	14	2.5	104	21	A71698	Human calcium chan
C 317	14	2.5	107	13	C35838	42 KD promoter. S
C 318	14	2.5	107	14	Q35405	AMEPV 42 KD promot
C 319	14	2.5	110	14	Q33138	AMEPV 42 K promote
C 320	14	2.5	115	21	A45604	Human secreted exp
C 321	14	2.5	119	16	T21518	Human gene signatu
C 322	14	2.5	125	17	T27866	Oligonucleotide se
C 323	14	2.5	129	16	T25190	Human gene signatu
C 324	14	2.5	132	21	C18469	Human secreted pro
C 325	14	2.5	135	17	T07239	Immunogen DNA from
C 326	14	2.5	150	4	N30069	Sequence of subseq
C 327	14	2.5	150	7	N60978	Fragment AI is a p
C 328	14	2.5	150	20	X05169	Human MSH5 (MMSH5)
C 329	14	2.5	172	21	C30131	Human secreted pro
C 330	14	2.5	178	21	C24722	Human secreted pro
C 331	14	2.5	181	21	Z89006	Human retina-spei
C 332	14	2.5	182	21	C13797	Human secreted pro
C 333	14	2.5	195	21	A69279	Bacteriophage Dp-1
C 334	14	2.5	204	21	C15762	Human secreted pro
C 335	14	2.5	205	17	T32989	Mouse neuropeptide
C 336	14	2.5	208	21	C27902	Human secreted pro
C 337	14	2.5	215	16	T25943	Human gene signatu
C 338	14	2.5	217	19	X12192	Human diallelic po
C 339	14	2.5	222	21	A42945	Human secreted exp
C 340	14	2.5	228	21	C21462	Human secreted pro
C 341	14	2.5	231	20	X41416	Human secreted pro
C 342	14	2.5	234	21	C17443	Human secreted pro
C 343	14	2.5	239	21	C04359	Human secreted pro
C 344	14	2.5	241	21	C00645	Human secreted pro
C 345	14	2.5	242	20	X40492	Human secreted pro
C 346	14	2.5	251	19	X11662	Human diallelic po
C 347	14	2.5	251	19	X12841	Human diallelic po
C 348	14	2.5	252	22	C90271	Partial mouse SNOR
C 349	14	2.5	256	16	T21908	Human gene signatu
C 350	14	2.5	257	21	C05901	Human secreted pro
C 351	14	2.5	265	21	A42012	Human secreted exp
C 352	14	2.5	271	21	C15080	Human secreted pro
C 353	14	2.5	274	16	T24164	Human gene signatu
C 354	14	2.5	278	21	C04249	Human gene signatu
C 355	14	2.5	289	21	Z42583	Human secreted pro
C 356	14	2.5	292	21	A45872	Human secreted exp
C 357	14	2.5	300	20	Z14563	Human gene express
C 358	14	2.5	300	21	A01189	Human colon cancer
C 359	14	2.5	300	21	A01306	Human colon cancer
C 360	14	2.5	301	18	V77372	Staphylococcus aur
C 361	14	2.5	301	21	C04627	Human secreted pro
C 362	14	2.5	301	21	A06483	Human immunogenic
C 363	14	2.5	302	21	C17281	Human secreted pro
C 364	14	2.5	305	20	Z10353	An intron/exon seq
C 365	14	2.5	305	21	C00517	Human secreted pro
C 366	14	2.5	306	20	X85728	Novel cDNA sequenc
C 367	14	2.5	311	21	C03592	Human secreted pro
C 368	14	2.5	311	21	C25061	Human secreted pro
C 369	14	2.5	314	21	A42039	Human secreted pro
C 370	14	2.5	322	16	T24879	Human gene signatu
C 371	14	2.5	333	21	A69234	Bacteriophage Dp-1
C 372	14	2.5	342	14	Q40891	T-BM gene sequenc
C 373	14	2.5	348	21	C28276	Human secreted pro
C 374	14	2.5	352	21	F21977	Human breast and o
C 375	14	2.5	359	21	C29367	Human secreted pro
C 376	14	2.5	394	21	C26408	Human secreted pro

377	14	2.5	395	21	A44539	Human secreted exp	c 450	14	2.5	650	20	V86942	EST clone BK61. H
378	14	2.5	399	21	C94093	Cat flea head and	451	14	2.5	650	21	Z80589	Human colon cancer
379	14	2.5	400	18	V75836	Staphylococcus aur	452	14	2.5	651	21	C54978	Arabidopsis thalia
380	14	2.5	400	18	V78383	Staphylococcus aur	453	14	2.5	653	21	C52439	Arabidopsis thalia
381	14	2.5	400	21	A26853	Essential Staphylo	454	14	2.5	654	21	F08474	Fusarium venenatum
382	14	2.5	402	21	F08639	Fusarium venenatum	455	14	2.5	655	21	C47698	Arabidopsis thalia
383	14	2.5	405	18	V75577	Staphylococcus aur	456	14	2.5	656	21	A98448	Roe deer PTEN/MMAC
384	14	2.5	406	21	C03312	Human secreted pro	457	14	2.5	657	21	A98859	Human proliferatio
385	14	2.5	407	21	C57423	Archidonic acid m	458	14	2.5	657	21	A98141	Human colon cancer
386	14	2.5	407	21	C57939	Synthetic DNA frag	459	14	2.5	667	21	Z80594	Arabidopsis thalia
387	14	2.5	420	20	X89751	Human secreted exp	460	14	2.5	672	21	F22110	Streptococcus pneu
388	14	2.5	430	21	A44086	Human secreted pro	461	14	2.5	680	18	X30844	Plnus radiata cati
389	14	2.5	432	21	C13324	Candida IFM5773 mi	462	14	2.5	682	21	T84074	Aspergillus oryzae
390	14	2.5	434	19	V22112	Staphylococcus aur	463	14	2.5	686	18	F14580	Interleukin 4 rece
391	14	2.5	439	18	V77953	Human secreted pro	464	14	2.5	688	21	V04437	Rat neuronal limed
392	14	2.5	441	21	C02544	Human secreted pro	465	14	2.5	696	18	V04437	Arabidopsis thalia
393	14	2.5	443	21	C27989	Human secreted pro	466	14	2.5	699	20	Z28259	Arabidopsis thalia
394	14	2.5	446	21	C27989	Human secreted pro	467	14	2.5	702	21	C48336	Arabidopsis thalia
395	14	2.5	449	19	V73606	H. pylori caga DNA	468	14	2.5	704	21	C34079	Arabidopsis thalia
396	14	2.5	450	21	C79348	Plant viral moveme	469	14	2.5	705	21	C46491	Arabidopsis thalia
397	14	2.5	454	21	C04071	Human secreted pro	470	14	2.5	707	21	C34713	Arabidopsis thalia
398	14	2.5	459	14	Q48618	Cpg depleted gpt g	471	14	2.5	711	21	A47148	Arabidopsis thalia
399	14	2.5	461	16	T19904	Human gene signalu	472	14	2.5	720	21	F12664	DNA encoding the m
400	14	2.5	464	16	O86543	Wilson disease exo	473	14	2.5	724	21	F11860	Aspergillus oryzae
401	14	2.5	472	21	C21427	Human secreted pro	474	14	2.5	725	21	Z97446	Human prostate can
402	14	2.5	475	7	N60226	Sequence encoding	475	14	2.5	728	21	C13858	Human gene express
403	14	2.5	475	20	V88421	EST clone EL360.	476	14	2.5	732	20	Z17594	Human prostate can
404	14	2.5	478	21	C43562	Zea mays DNA fragm	477	14	2.5	746	21	Z97445	Human gene express
405	14	2.5	479	21	F11130	Fusarium venenatum	478	14	2.5	748	21	A78518	Human prostate can
406	14	2.5	487	21	A57265	Human breast cance	479	14	2.5	749	20	Z17441	Human gene express
407	14	2.5	488	21	C37257	Arabidopsis thalia	480	14	2.5	752	21	A78486	Plant SDF polynuci
408	14	2.5	489	21	C44316	Arabidopsis thalia	481	14	2.5	756	20	X99513	Human gene express
409	14	2.5	489	21	C10151	Human secreted pro	482	14	2.5	759	20	X99513	Nucleic acid seque
410	14	2.5	491	21	C36609	Arabidopsis thalia	483	14	2.5	760	22	F22467	Human breast cance
411	14	2.5	498	21	F10963	Fusarium venenatum	484	14	2.5	768	20	Z33517	Human validated ca
412	14	2.5	505	20	V86428	EST clone AR467.	485	14	2.5	774	20	X99052	Human validated ca
413	14	2.5	513	20	V87757	EST clone BQ207.	486	14	2.5	777	19	X14303	H. pylori GHP0 70
414	14	2.5	514	18	T80799	Staphylococcus aur	487	14	2.5	783	19	V38999	Exemplary CD40 lig
415	14	2.5	515	18	X20817	Polynucleotide seq	488	14	2.5	783	19	V42184	Exemplary nucleoti
416	14	2.5	517	20	X20846	Polynucleotide seq	489	14	2.5	783	21	C39655	Arabidopsis thalia
417	14	2.5	523	21	C55705	Human differential	490	14	2.5	786	15	O63959	Human CD40-L type
418	14	2.5	524	20	Z09015	Differentiation in	491	14	2.5	786	19	V46279	A. thaliana NIM-1
419	14	2.5	525	21	F14765	Aspergillus oryzae	492	14	2.5	786	19	V38997	CD40 ligand gene u
420	14	2.5	526	21	C34077	Arabidopsis thalia	493	14	2.5	786	19	V39002	Exemplary CD40 lig
421	14	2.5	543	20	X20858	Polynucleotide seq	494	14	2.5	786	19	V43665	Non-Inducible Immu
422	14	2.5	548	21	C71142	Single nucleotide	495	14	2.5	786	19	V12852	CD40 ligand coding
423	14	2.5	549	21	C93877	Cat flea hindgut a	496	14	2.5	786	21	A01868	Human colon cancer
424	14	2.5	549	21	C94364	Cat flea head and	497	14	2.5	791	19	V53452	DNA encoding a Sta
425	14	2.5	549	21	C94811	Enterococcus faeca	498	14	2.5	798	18	V74928	Staphylococcus aur
426	14	2.5	553	20	X13524	DNA encoding a Sta	499	14	2.5	798	20	Z77451	Human ovarian tumo
427	14	2.5	557	18	T83802	Human secreted pro	500	14	2.5	799	21	C38896	Arabidopsis thalia
428	14	2.5	574	21	C00999	Single nucleotide	501	14	2.5	822	20	X84978	Human fetal placen
429	14	2.5	578	21	C72664	Single nucleotide	502	14	2.5	839	21	A40576	CD40-L. DNA. Homo
430	14	2.5	578	21	C72685	Single nucleotide	503	14	2.5	840	14	O41506	Genomic sequence o
431	14	2.5	578	21	C72694	Arabidopsis thalia	504	14	2.5	840	15	O57984	CD40 ligand gene.
432	14	2.5	581	21	C52354	Arabidopsis thalia	505	14	2.5	840	15	O67123	Human CD40-L. CDNA.
433	14	2.5	585	21	A15914	Human protein clon	506	14	2.5	840	16	T05763	Human CD40-L. CDNA.
434	14	2.5	585	22	C92249	PERV-MSN1 pol regi	507	14	2.5	840	16	O94091	CDNA of CD40L, a n
435	14	2.5	586	21	A16134	Human colon cancer	508	14	2.5	840	18	T93782	Human CD40L. mutcin
436	14	2.5	586	22	C92248	PERV-MSN1 pol regi	509	14	2.5	840	18	T58132	S. pneumoniae dert
437	14	2.5	590	21	C50370	Arabidopsis thalia	510	14	2.5	840	19	Z96467	Human CD40-L. codin
438	14	2.5	590	22	C92250	PERV-MSN1 pol regi	511	14	2.5	840	19	V61053	Human SDF polynuci
439	14	2.5	593	18	X30892	Streptococcus pneu	512	14	2.5	840	20	Z27525	Plant SDF polynuci
440	14	2.5	593	21	C34261	Arabidopsis thalia	513	14	2.5	866	21	A78488	H. pylori GHP0 170
441	14	2.5	600	20	V86185	EST clone J635. H	514	14	2.5	880	19	X14588	Replication initia
442	14	2.5	603	18	T67670	H. pylori cytoplas	515	14	2.5	889	11	O04528	DNA encoding a S.
443	14	2.5	606	19	V42183	Exemplary nucleoti	516	14	2.5	894	19	T98730	Arabidopsis thalia
444	14	2.5	609	6	N50090	Sequence encoding	517	14	2.5	900	7	C37201	0.9 Kbp segment of
445	14	2.5	620	16	T05790	Human CD40 ligand	518	14	2.5	900	17	N60506	KSHV assembly prot
446	14	2.5	620	21	C45159	Arabidopsis thalia	519	14	2.5	900	18	V09008	Staphylococcus aur
447	14	2.5	621	20	X99586	Nucleic acid seque	520	14	2.5	904	16	V74321	Sequence encoding
448	14	2.5	641	21	D00433	Human MIM15 DNA c	521	14	2.5	906	11	O05975	Human cancer assoc
449	14	2.5	642	19	X30601	H. pylori cellular	522	14	2.5	906	21	C77681	

523	14	2.5	908	21	C74382	Human secreted pro
C 524	14	2.5	914	21	C47666	Arabidopsis thalia
C 525	14	2.5	915	19	V09009	KSHV assembly prot
526	14	2.5	919	18	V74871	Staphylococcus aur
C 527	14	2.5	923	21	C42604	Arabidopsis thalia
C 528	14	2.5	930	17	T36784	Prostate-specific
529	14	2.5	932	20	V84771	Human secreted pro
C 530	14	2.5	941	13	Q29856	Odorant receptor c
C 531	14	2.5	975	21	C42291	Arabidopsis thalia
C 532	14	2.5	979	21	A94088	Fruit-associated b
C 533	14	2.5	989	21	A50292	Candida albicans C
C 534	14	2.5	997	21	C45393	Arabidopsis thalia
535	14	2.5	1000	20	Z15900	Human gene express
536	14	2.5	1000	20	Z15901	Human gene express
C 537	14	2.5	1001	22	C88189	Optimum primer can
C 538	14	2.5	1009	21	C41101	Arabidopsis thalia
C 539	14	2.5	1015	16	T04076	M.gallisepticum DN
540	14	2.5	1017	17	T41625	Adzuki bean xylogl
541	14	2.5	1018	14	Q36929	HEV1 cDNA clone.
C 542	14	2.5	1024	21	Z97146	Human prostate can
543	14	2.5	1025	9	N80304	Sequence of cDNA c
544	14	2.5	1030	21	C78042	Human cancer assoc
545	14	2.5	1031	22	C90276	Mouse SNORF3 rece
546	14	2.5	1035	16	T04705	PC3POLY1A fragmen
C 547	14	2.5	1036	20	Z17349	Human gene express
C 548	14	2.5	1037	20	X84975	Human secreted pro
549	14	2.5	1047	18	T84182	DNA encoding a sta
550	14	2.5	1047	19	V53521	DNA encoding a sta
551	14	2.5	1049	21	C37987	Arabidopsis thalia
C 552	14	2.5	1054	11	Q06112	Sequence encoding
C 553	14	2.5	1070	18	T59195	Clone PT218 contai
C 554	14	2.5	1070	20	Z29901	Nucleotide sequenc
C 555	14	2.5	1070	21	Z48591	N. tabacum cryptic
C 556	14	2.5	1074	21	A94091	Fusion sequence of
557	14	2.5	1076	21	A68179	Bacteriophage Dp-1
C 558	14	2.5	1079	17	T36068	Chicken gamma inte
C 559	14	2.5	1081	21	A97924	A. thaliana PUP1 D
560	14	2.5	1087	20	X19424	Nicotiana tabacum
C 561	14	2.5	1096	19	V07891	Nucleotide sequenc
562	14	2.5	1101	22	C90246	Rat SNORF3 recept
563	14	2.5	1106	13	Q29663	Sugar beet acidic
C 564	14	2.5	1111	11	Q05671	Uncoupling protein
C 565	14	2.5	1111	11	Q08578	UCP messenger RNA.
C 566	14	2.5	1115	10	N90125	cDNA encoding IGE
C 567	14	2.5	1119	21	C53578	Arabidopsis thalia
568	14	2.5	1127	17	T41618	Adzuki bean xylogl
C 569	14	2.5	1127	20	Z21221	Zea mays eIF-4E pr
570	14	2.5	1128	20	Z24655	Human lung tumor a
571	14	2.5	1128	21	C65894	Human lung cancer-
572	14	2.5	1128	21	C46094	Arabidopsis thalia
573	14	2.5	1130	21	C31166	Arabidopsis thalia
574	14	2.5	1131	21	C76646	Human ORF ORF2201
575	14	2.5	1139	11	Q06249	Phospholipase D to
576	14	2.5	1140	21	C33314	Arabidopsis thalia
577	14	2.5	1141	21	C51073	Arabidopsis thalia
C 578	14	2.5	1149	21	A39968	Murine TANGO 186 c
C 579	14	2.5	1155	21	C49626	Arabidopsis thalia
C 580	14	2.5	1156	20	X76974	Histamine binding
C 581	14	2.5	1159	21	C39510	Arabidopsis thalia
582	14	2.5	1173	15	Q67883	Murine p53 DNA. S
583	14	2.5	1173	20	Z32518	Mouse p53 gene.
584	14	2.5	1173	20	Z08528	Murine p53 gene.
C 585	14	2.5	1174	21	C52054	Arabidopsis thalia
C 586	14	2.5	1175	11	Q04088	Bod4-15 insert enc
587	14	2.5	1175	21	A05567	Streptococcus pneu
C 588	14	2.5	1176	20	X61405	DNA encoding a hum
C 589	14	2.5	1194	18	V74433	Staphylococcus aur
590	14	2.5	1194	19	V46278	A. thaliana C- and
591	14	2.5	1194	19	V43664	Non-inducible immu
C 592	14	2.5	1194	21	Z51529	S. paucimobilis am
593	14	2.5	1202	13	Q25060	PSbeta1a-318 clone
C 594	14	2.5	1212	20	Z28298	Rat neuronal immed
595	14	2.5	1217	21	A51362	Streptococcus agal
596	14	2.5	1220	20	X84956	Human secreted pro
C 597	14	2.5	1223	18	V74891	Staphylococcus aur
C 598	14	2.5	1225	22	F44488	Mouse dextran sodi
C 599	14	2.5	1231	20	Z28265	Rat neuronal immed
600	14	2.5	1234	21	C77698	Human cancer assoc
601	14	2.5	1234	21	C49818	Arabidopsis thalia
C 602	14	2.5	1235	14	Q33062	Encodes Babesia bo
C 603	14	2.5	1235	17	T18993	Babesia merozoit
604	14	2.5	1242	21	C79768	Human secreted pro
605	14	2.5	1247	21	C35991	Arabidopsis thalia
606	14	2.5	1271	18	T95020	Arabidopsis JAG18
C 607	14	2.5	1281	21	C43477	Arabidopsis thalia
C 608	14	2.5	1286	21	C56341	Pinus radiata tran
C 609	14	2.5	1293	21	C45019	Arabidopsis thalia
C 610	14	2.5	1303	21	A95345	Aspergillus polyke
611	14	2.5	1310	20	Z24656	Human lung tumor a
612	14	2.5	1310	21	C65895	Human lung cancer-
613	14	2.5	1317	15	Q71601	Japanese cedar pol
C 614	14	2.5	1333	21	C44915	Arabidopsis thalia
615	14	2.5	1337	14	Q35304	Cry j I gene. Cry
616	14	2.5	1337	15	O55271	Cry j I gene. Cry
617	14	2.5	1337	16	T04248	Cry j I Japanese C
C 618	14	2.5	1343	22	F33131	Human secreted pro
619	14	2.5	1348	21	F18332	Lung cancer associ
620	14	2.5	1349	21	Z24205	S. aureus sarA reg
C 621	14	2.5	1353	17	T41701	Murine lymphocyte
622	14	2.5	1356	21	Z39863	Plasmodium malaria
623	14	2.5	1358	18	T84705	Human renin cDNA.
624	14	2.5	1368	21	C49566	Arabidopsis thalia
C 625	14	2.5	1368	14	Q38448	Arabidopsis thalia
626	14	2.5	1372	21	C33629	Arabidopsis thalia
C 627	14	2.5	1375	21	C51920	Arabidopsis thalia
C 628	14	2.5	1378	21	C42223	Arabidopsis thalia
629	14	2.5	1387	14	O53419	Mycoplasma gallise
630	14	2.5	1387	15	Q77854	Mycoplasma gallise
631	14	2.5	1387	16	Q94711	Mycoplasma gallise
632	14	2.5	1388	17	T18168	COR1 potassium cha
633	14	2.5	1389	12	Q14918	CD46 clone pm5.3.
634	14	2.5	1389	20	Z17120	Human gene express
635	14	2.5	1395	21	C75776	Human ORF ORF1331
636	14	2.5	1396	21	C54561	Arabidopsis thalia
637	14	2.5	1401	18	T95022	Arabidopsis thalia
638	14	2.5	1401	21	C33196	DNA flanking the T
639	14	2.5	1419	21	C49392	Arabidopsis thalia
640	14	2.5	1419	21	C49393	Arabidopsis thalia
641	14	2.5	1425	21	F11620	Aspergillus niger
642	14	2.5	1431	12	Q14917	CD46 clone pm5.10.
643	14	2.5	1441	19	V43594	Arabidopsis chloro
644	14	2.5	1443	18	T80793	Staphylococcus aur
645	14	2.5	1443	19	V53427	DNA encoding a sta
646	14	2.5	1455	21	C46079	Arabidopsis thalia
647	14	2.5	1457	21	C33676	Arabidopsis thalia
648	14	2.5	1459	6	N50180	Sequence encoding
649	14	2.5	1463	21	C39968	Arabidopsis thalia
C 650	14	2.5	1472	21	C50136	Arabidopsis thalia
651	14	2.5	1477	18	T90306	Human MCP cDNA. H
C 652	14	2.5	1477	21	C33778	Arabidopsis thalia
653	14	2.5	1484	19	V18254	Human growth-induc
654	14	2.5	1497	21	C40181	Arabidopsis thalia
C 655	14	2.5	1505	18	T72177	Alzheimer's diseas
656	14	2.5	1505	21	C47413	Arabidopsis thalia
657	14	2.5	1510	21	C34975	Arabidopsis thalia
658	14	2.5	1512	19	V68995	DNA molecule encod
659	14	2.5	1512	21	C81006	Human BILAG1 anti
660	14	2.5	1512	21	A06593	Human immunogeni
661	14	2.5	1515	21	A70162	Plasmodium falcipa
662	14	2.5	1515	21	C50415	Arabidopsis thalia
C 663	14	2.5	1523	21	A02658	Human colon cancer
664	14	2.5	1523	21	C38003	Arabidopsis thalia
665	14	2.5	1530	16	Q99106	Human MCP (CD46) F
666	14	2.5	1530	16	T03339	Human CD46 cDNA.
C 667	14	2.5	1533	18	T87066	Bovine platelet-ac
668	14	2.5	1533	20	X08478	Bovine plasma plat

C 669	14	2.5	1533	20	V08552	Bovine PAF-AH codi	C 742	14	2.5	1863	21	Z48290	Bacillus sp. A386
C 670	14	2.5	1533	21	A59594	cDNA encoding plat	C 743	14	2.5	1874	21	A57959	1875 bp Candida al
C 671	14	2.5	1533	21	C45930	Arabidopsis thalia	C 744	14	2.5	1874	22	F32659	Human secreted pro
C 672	14	2.5	1533	21	A10879	Bovine PAF-AH nucl	C 745	14	2.5	1917	21	Z87219	DNA encoding nativ
C 673	14	2.5	1533	21	Z24255	Bovine PAF-AH cDNA	C 746	14	2.5	1923	21	C47422	Arabidopsis thalia
C 674	14	2.5	1533	22	C89072	Platelet-activatin	C 747	14	2.5	1925	21	A94092	Arabidopsis thalia
C 675	14	2.5	1539	21	C35232	Arabidopsis thalia	C 748	14	2.5	1925	21	C38450	Fusion sequence of
C 676	14	2.5	1539	21	C42990	Arabidopsis thalia	C 749	14	2.5	1931	19	Z96385	S. pneumoniae deriv
C 677	14	2.5	1542	21	C45040	Arabidopsis thalia	C 750	14	2.5	1933	21	A23442	cDNA encoding huma
C 678	14	2.5	1546	21	C34726	Arabidopsis thalia	C 751	14	2.5	1943	7	N60965	Autonomously repli
C 679	14	2.5	1551	12	Q10864	Sequence encoding	C 752	14	2.5	1948	21	A09312	Human cancer assoc
C 680	14	2.5	1556	20	V48612	Human secreted pro	C 753	14	2.5	1950	20	X86149	DNA encoding a Bac
C 681	14	2.5	1564	20	Z08962	Human neckine-1 cD	C 754	14	2.5	1962	20	Z52334	Human prostate tum
C 682	14	2.5	1579	17	T74594	AT1g cDNA involved	C 755	14	2.5	1962	20	Z52334	Human prostate tum
C 683	14	2.5	1590	19	V09014	KSHV protease/asse	C 756	14	2.5	1975	11	Q05057	DraI/DraI fragment
C 684	14	2.5	1594	21	C53583	Arabidopsis thalia	C 757	14	2.5	1977	17	T36794	Prostate-specific
C 685	14	2.5	1597	19	V46276	A. thaliana N-term	C 758	14	2.5	1980	20	X40197	Sequence of C3Vs g
C 686	14	2.5	1597	19	V43662	Non-inducible immu	C 759	14	2.5	1986	7	N60595	2.0 kbp segment of
C 687	14	2.5	1605	19	V09016	KSHV protease/asse	C 760	14	2.5	1991	12	Q14916	CD46 clone pms.6.
C 688	14	2.5	1608	19	V46277	A. thaliana C-term	C 761	14	2.5	1992	14	Q48591	Alcohol oxidase ge
C 689	14	2.5	1608	19	V43663	Non-inducible immu	C 762	14	2.5	2001	18	T59700	PTH-like peptide D
C 690	14	2.5	1608	21	A57988	1608 bp Candida al	C 763	14	2.5	2001	21	A26941	Essential Staphylo
C 691	14	2.5	1608	21	Z46680	Human IFN-gamma DN	C 764	14	2.5	2007	21	A39967	Murine TANGO 186 c
C 692	14	2.5	1608	22	C87635	Bovine beta-1,4-N-	C 765	14	2.5	2011	19	V46274	Murine NTM-1
C 693	14	2.5	1610	18	M59911	Yeast transcriptio	C 766	14	2.5	2011	19	V46275	A. thaliana NTM-1
C 694	14	2.5	1610	21	C79774	Human secreted pro	C 767	14	2.5	2011	19	V43661	Non-inducible immu
C 695	14	2.5	1619	20	X13500	Enterococcus faeca	C 768	14	2.5	2023	21	C49400	Arabidopsis thalia
C 696	14	2.5	1622	18	V75043	Staphylococcus aur	C 769	14	2.5	2024	21	C37765	Arabidopsis thalia
C 697	14	2.5	1627	20	X13633	Enterococcus faeca	C 770	14	2.5	2040	21	A52773	Soybean putative c
C 698	14	2.5	1629	21	C48405	Arabidopsis thalia	C 771	14	2.5	2042	21	C41973	Arabidopsis thalia
C 699	14	2.5	1630	20	Z42039	Human endometrium	C 772	14	2.5	2043	20	X59526	DNA encoding the b
C 700	14	2.5	1630	20	Z42039	Human endometrium	C 773	14	2.5	2044	21	Z43754	Murine NNX3 cDNA.
C 701	14	2.5	1631	19	X14344	H. pylori GHP0 265	C 774	14	2.5	2065	22	F32645	Human cDNA encodin
C 702	14	2.5	1638	20	X84991	Human secreted pro	C 775	14	2.5	2071	19	V46494	Interleukin-1 beta
C 703	14	2.5	1639	18	V74661	Staphylococcus aur	C 776	14	2.5	2076	21	A09044	Fusion polypeptide
C 704	14	2.5	1643	21	A87754	Human secreted pro	C 777	14	2.5	2084	21	Z52492	Fusion polypeptide
C 705	14	2.5	1643	21	Z56150	Human Cathepsin S	C 778	14	2.5	2085	21	A09043	Fusion polypeptide
C 706	14	2.5	1659	12	Q14915	CD46 clone pms.1.	C 779	14	2.5	2085	21	A09045	Arabidopsis thalia
C 707	14	2.5	1659	21	C69476	Human secreted pro	C 780	14	2.5	2105	21	V16851	A. thaliana gene 1
C 708	14	2.5	1668	21	A712926	At1gplex gmelini N	C 781	14	2.5	2105	19	V38373	Beta(1 -> 4)-N-ace
C 709	14	2.5	1685	20	Z34205	Human PRO273 nucle	C 782	14	2.5	2115	19	V38373	1-Sucrose:sucrose
C 710	14	2.5	1685	21	C78551	Human PRO273 (UNO2-	C 783	14	2.5	2116	17	T31024	Varicella Zoster V
C 711	14	2.5	1685	21	C58588	Human PRO273 prote	C 784	14	2.5	2133	17	Q14966	A. thaliana shorte
C 712	14	2.5	1689	20	Z40803	Secreted protein E	C 785	14	2.5	2134	22	C84186	Mouse GP88 autocri
C 713	14	2.5	1690	20	X04614	Genomic sequence e	C 786	14	2.5	2137	20	V82824	Pea DR206 protein
C 714	14	2.5	1701	19	V09015	KSHV protease/asse	C 787	14	2.5	2140	21	Z49411	Human secreted pro
C 715	14	2.5	1710	21	C39470	Arabidopsis thalia	C 788	14	2.5	2158	21	C93483	S. thermophilus FI
C 716	14	2.5	1719	16	Q91211	TF55 molecular cha	C 789	14	2.5	2161	19	V29573	Human SVPH1-26 pro
C 717	14	2.5	1750	20	X30400	DNA encoding a hum	C 790	14	2.5	2181	20	X56461	cDNA encoding a hu
C 718	14	2.5	1752	21	C75773	Human ORFX ORF1328	C 792	14	2.5	2204	21	Z43753	Human NNX3 cDNA.
C 719	14	2.5	1760	21	C59930	Human secreted pro	C 793	14	2.5	2207	20	X03845	Partial human 7-rr
C 720	14	2.5	1767	21	C46909	Arabidopsis thalia	C 794	14	2.5	2220	20	O33008	Novel intestinal o
C 721	14	2.5	1776	18	T67912	H. pylori cytoplas	C 795	14	2.5	2222	18	V74983	Staphylococcus aur
C 722	14	2.5	1779	21	A49185	cDNA encoding huma	C 796	14	2.5	2222	18	V74983	Human endometrium
C 723	14	2.5	1781	21	C50268	Arabidopsis thalia	C 797	14	2.5	2236	19	V38368	Beta(1 -> 4)-N-ace
C 724	14	2.5	1785	20	X99656	Nucleic acid seque	C 798	14	2.5	2259	21	C42350	40 kDa and 34 kDa
C 725	14	2.5	1789	20	Z41984	Human endometrium	C 799	14	2.5	2259	21	C42350	Arabidopsis thalia
C 726	14	2.5	1801	21	C36220	Arabidopsis thalia	C 800	14	2.5	2267	21	C59489	Human secreted pro
C 727	14	2.5	1813	21	C39494	Arabidopsis thalia	C 801	14	2.5	2276	18	T84929	Human prostate pro
C 728	14	2.5	1816	21	A51745	Human CbD0 ligand	C 802	14	2.5	2276	18	T84929	cDNA encoding a pr
C 729	14	2.5	1821	19	V22736	Babesia microti BM	C 803	14	2.5	2292	21	A05501	Streptococcus pneu
C 730	14	2.5	1821	20	X89000	B. microti BMN1-6	C 804	14	2.5	2294	18	T60957	Maize tapetum-spec
C 731	14	2.5	1821	21	C65083	Human secreted pro	C 805	14	2.5	2302	15	C76368	Human ORFX ORF1923
C 732	14	2.5	1827	21	F22379	DNA molecule encod	C 807	14	2.5	2309	15	C73786	Partial PCR fragme
C 733	14	2.5	1838	21	C59703	Human secreted pro	C 808	14	2.5	2332	20	X03844	Human 7-transmembr
C 734	14	2.5	1853	19	V68996	DNA molecule encod	C 809	14	2.5	2346	15	X80866	Human nucleic acid
C 735	14	2.5	1853	21	A06594	Human B11ag1 antlg	C 810	14	2.5	2346	15	X80866	DNA encoding huma
C 736	14	2.5	1853	21	A06594	Human B11ag1 antlg	C 811	14	2.5	2354	21	Z50348	Mycoplasma gallise
C 737	14	2.5	1855	19	V68998	DNA molecule encod	C 812	14	2.5	2354	21	Z50348	Human secreted pro
C 738	14	2.5	1855	19	V57301	Mize cell death s	C 813	14	2.5	2355	20	A09049	IL-13/IL-4 dual tr
C 739	14	2.5	1855	21	C81009	Human B11ag1 antlg	C 814	14	2.5	2356	20	X90696	Human Cytoplasmic
C 740	14	2.5	1855	21	A06596	Human immunogenic							
C 741	14	2.5	1862	21	A59972	Bovine calcatenin							

Bacillus sp. A3866
1875 bp Candida albicans
Human secreted protein
DNA encoding native
Arabidopsis thaliana
Fusion sequence of
Arabidopsis thaliana
S. pneumoniae derived
cDNA encoding human
Autonomously repli
Human cancer assoc
DNA encoding a Bac
Human prostate tum
Human prostate tum
Drai/Drai fragment
Prostate-specific
Sequence of cDNA
2.0 kbp segment of
CD6 clone pmw.6.
Alcohol oxidase ge
PTH-like peptide b
Essential staphylo
Murine TANGO 186 c
A. thaliana NM-1
A. thaliana NM-1
Non-inducible immu
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Soybean putative c
Arabidopsis thaliana
DNA encoding the h
Murine NNK3 cDNA.
Human cDNA encodi
Interleukin-1 beta
Fusion polypeptide
Human secreted pro
Fusion polypeptide
Fusion polypeptide
Arabidopsis thaliana
Arabidopsis thaliana
A. thaliana gene 1
Beta1 -> 4'-N-ac
1-Sucrose:sucrose
Vaticella Zoster V
A. thaliana shorte
Mouse GP86 autocl
pea DRP206 protein
Human secreted pro
S. thermophilus FI
Human SVPH1-26 pro
cDNA encoding a hu
Human NNK3 cDNA.
Partial human 7-rr
Novel intestinal o
Staphylococcus aur
Human endometrium
Beta1 -> 4'-N-ac
40 kDa and 34 kDa
Arabidopsis thaliana
Human secreted pro
cDNA encoding a pro
Streptococcus pneu
Streptococcus pneu
Maize taletum-spec
Human ORF19233
Partial PCR fragme
Human 7-transmembr
Human nucleic acid
DNA encoding human
Mycoplasma gallise
Human secreted pro
Human secreted pro
Human 13/IL-4 dual
Human Cytoplasmic

C 815	14	2.5	2374	18	T96816	DNA encoding LysC, IL-13/IL-4 dual tr	C 888	14	2.5	2999	21	C78119	Human cancer assoc
C 816	14	2.5	2382	21	A09050	CDNA encoding an a	C 889	14	2.5	3000	20	X06828	Chlamydia pneumoni
C 817	14	2.5	2393	21	Z46135	Staphylococcus aure	C 890	14	2.5	3024	14	O39260	ICAM-1 cDNA. Homo
C 818	14	2.5	2400	20	X25372	Humicola insolens	C 891	14	2.5	3035	19	X14059	H. pylori GHPo 325
C 819	14	2.5	2409	19	V19377	H. insolens celluli	C 892	14	2.5	3042	19	V25285	Recombinant botuli
C 820	14	2.5	2409	19	V19281	Nucleotide sequenc	C 893	14	2.5	3058	20	X90695	Human Cytoplasmic
C 821	14	2.5	2426	20	X28636	Enterococcus faeca	C 894	14	2.5	3065	10	N91438	DNA encoding glyci
C 822	14	2.5	2441	15	O55144	CDNA encoding a hu	C 895	14	2.5	3091	21	C99028	Murine wild type p
C 823	14	2.5	2449	21	A63952	Fruit-associated b	C 896	14	2.5	3097	17	T28951	Human pancreatic c
C 824	14	2.5	2453	21	A94087	Human ORF ORF1426	C 897	14	2.5	3126	14	O42425	ADAR DNA. Synthe
C 825	14	2.5	2459	21	C75871	CDNA encoding a hu	C 898	14	2.5	3140	21	V29814	Subtilase (St_P25c
C 826	14	2.5	2459	21	A12406	Coding region of h	C 899	14	2.5	3159	18	V74614	Staphylococcus aur
C 827	14	2.5	2470	18	T72944	Human interleukin-	C 900	14	2.5	3172	22	C84184	Nucleotide sequenc
C 828	14	2.5	2475	11	O04307	Human interleukin-	C 901	14	2.5	3184	22	C84184	A. thaliana larger
C 829	14	2.5	2475	18	T61551	Human interleukin-	C 902	14	2.5	3214	5	N40244	Hepatitis virus ad
C 830	14	2.5	2475	19	V38331	Human IL-4 recepto	C 903	14	2.5	3215	11	O05377	Fragment of plasm
C 831	14	2.5	2475	19	V17656	Human IL-4 recepto	C 904	14	2.5	3215	21	T37088	Nucleotide sequenc
C 832	14	2.5	2475	20	X22408	Human Interleukin-	C 905	14	2.5	3218	18	T60328	Beta-casein promot
C 833	14	2.5	2475	20	V08857	Coding sequence fo	C 906	14	2.5	3218	18	V74747	Staphylococcus aur
C 834	14	2.5	2487	20	X38813	Pinus radiata cell	C 907	14	2.5	3288	16	T05055	Human transforming
C 835	14	2.5	2513	21	A79275	DNA encoding a mem	C 908	14	2.5	3308	21	F18270	Lung cancer associ
C 836	14	2.5	2520	21	A46789	Soluble Interleuk	C 909	14	2.5	3350	21	Z40700	Human EGFR polype
C 837	14	2.5	2520	21	Z50939	Human secreted pro	C 910	14	2.5	3355	20	X36342	Human TIE ligand N
C 838	14	2.5	2532	21	Z98026	DNA encoding nativ	C 911	14	2.5	3355	21	A75529	Human PRO188 cDNA
C 839	14	2.5	2532	21	Z87218	Human activated le	C 912	14	2.5	3355	22	C97379	Human angio genesis
C 840	14	2.5	2539	17	T46075	Activated leukocyt	C 913	14	2.5	3411	17	T28950	Helicobacter-speci
C 841	14	2.5	2539	19	V13954	Nucleotide sequenc	C 914	14	2.5	3423	21	C45759	Arabidopsis thalia
C 842	14	2.5	2541	21	A59346	Human B3 ubiqutin	C 915	14	2.5	3508	21	A16619	Human secreted pro
C 843	14	2.5	2546	18	T72941	Human B3 ubiqutin	C 916	14	2.5	3539	18	T47537	Human secreted cyt
C 844	14	2.5	2559	20	Z05236	Neuronal activity-	C 917	14	2.5	3546	21	C42844	Arabidopsis thalia
C 845	14	2.5	2569	18	T88850	Botulinum neurotox	C 918	14	2.5	3550	18	T72946	Phaffia carotenoid
C 846	14	2.5	2613	19	V26280	Recombinant botuli	C 919	14	2.5	3555	22	F27737	Human transport pr
C 847	14	2.5	2616	19	V26291	Recombinant botuli	C 920	14	2.5	3561	15	O67667	Delta endotoxin ge
C 848	14	2.5	2616	19	V26291	Recombinant botuli	C 921	14	2.5	3561	18	T89184	Nematoe toxin 807
C 849	14	2.5	2622	19	V26288	Human ovarian tumo	C 922	14	2.5	3561	18	T77277	Bacillus thuringie
C 850	14	2.5	2627	20	Z77559	Recombinant botuli	C 923	14	2.5	3561	18	T61017	Bacillus thuringie
C 851	14	2.5	2628	19	V26281	Recombinant botuli	C 924	14	2.5	3567	21	A70117	Plasmodium falcipa
C 852	14	2.5	2637	19	V26282	Arabidopsis thalia	C 925	14	2.5	3580	20	V81742	Human PRP4 encodi
C 853	14	2.5	2646	21	C42283	42K promoted cytom	C 926	14	2.5	3592	21	A26912	Essential staphylo
C 854	14	2.5	2651	18	T47539	Enterococcus faeca	C 927	14	2.5	3597	21	F20977	Human low adenosin
C 855	14	2.5	2651	20	X13369	Human ORFX ORF2701	C 928	14	2.5	3597	21	A34855	Human adenosine re
C 856	14	2.5	2674	21	C77146	Human ORFX ORF2701	C 929	14	2.5	3600	20	X25180	Hiv-1 group O isol
C 857	14	2.5	2685	19	V26287	Recombinant botuli	C 930	14	2.5	3616	19	V00245	Rat Ret ligand ret
C 858	14	2.5	2724	19	V26284	Human EXCS encodin	C 931	14	2.5	3649	6	N50416	Calf acetyl cholin
C 859	14	2.5	2730	22	C84293	Human breast tumo	C 932	14	2.5	3654	16	T72326	Lactobacillus bact
C 860	14	2.5	2730	22	C84293	Chlamydia antigen	C 933	14	2.5	3661	16	T05902	Human IL-2 gene (p
C 861	14	2.5	2784	21	A30850	Mucor cancer assoc	C 934	14	2.5	3691	20	Z06408	Tumour suppressor
C 862	14	2.5	2804	21	C77708	Mucor cinctinelloid	C 935	14	2.5	3691	20	X99691	Nucleic acid sequ
C 863	14	2.5	2807	21	A11389	Chlamydia pneumoni	C 936	14	2.5	3692	20	Z27237	Human secreted pro
C 864	14	2.5	2815	20	X06817	Human secreted pro	C 937	14	2.5	3705	21	A53826	Sequence encoding
C 865	14	2.5	2820	21	C79730	Protein PR0228 cDN	C 938	14	2.5	3711	21	C77143	Human ORFX ORF2698
C 866	14	2.5	2822	20	X52222	PRO228 cDNA. Homo	C 939	14	2.5	3714	21	A51777	S. cerevisiae esse
C 867	14	2.5	2822	21	A54097	PRO228 cDNA. Homo	C 940	14	2.5	3738	21	A70178	Plasmodium falcipa
C 868	14	2.5	2822	21	Z93701	Human angio genesis	C 941	14	2.5	3747	21	C49587	Arabidopsis thalia
C 869	14	2.5	2822	22	C97429	Canine B7-1 protei	C 942	14	2.5	3792	21	C88443	Thiamine respons
C 870	14	2.5	2830	20	Z27909	Canine B7-1 gene c	C 943	14	2.5	3815	18	T84154	DNA encoding one k
C 871	14	2.5	2830	20	Z27910	Human cancer assoc	C 944	14	2.5	3815	19	V53496	Human encoding a Sta
C 872	14	2.5	2853	21	C77970	2858 bp Candida al	C 945	14	2.5	3822	20	X91737	Porphyromonas ging
C 873	14	2.5	2858	21	A58011	Recombinant botuli	C 946	14	2.5	3822	20	X91737	Nucleotide sequenc
C 874	14	2.5	2862	19	V26283	Mouse bone morphog	C 947	14	2.5	3833	21	A59529	Sequence of hepati
C 875	14	2.5	2875	18	T47713	Human pancreatic c	C 948	14	2.5	3846	20	X91736	Porphyromonas ging
C 876	14	2.5	2934	21	C98826	Human secreted pro	C 949	14	2.5	3853	21	C77598	Human ORFX ORF3153
C 877	14	2.5	2937	21	C59340	A. thaliana trehal	C 950	14	2.5	3891	17	T29244	C. botulinum type
C 878	14	2.5	2940	20	V65173	Human Rab3-GAP gen	C 951	14	2.5	3936	20	X91609	Porphyromonas ging
C 879	14	2.5	2946	20	V34005	S. aureus D-alanin	C 952	14	2.5	3936	21	A38929	Cotton delta-cadin
C 880	14	2.5	2948	20	V08568	Chlamydia antigen	C 953	14	2.5	4002	21	Z24153	Murine PG-Lb DNA.
C 881	14	2.5	2950	21	A30849	CDNA encoding huma	C 954	14	2.5	4071	18	T68658	Sequence of introm
C 882	14	2.5	2969	21	A23450	Borrelia burgdorfe	C 955	14	2.5	4144	14	O37188	Mycoplasma pneumo
C 883	14	2.5	2970	20	X20290	Human SGP cDNA.	C 956	14	2.5	4184	19	V41259	Mouse FosB coding
C 884	14	2.5	2987	21	Z94785	FLPV matrix (M) ge	C 957	14	2.5	4193	16	O82834	Mouse neuronal PAS
C 885	14	2.5	2989	18	T69956	Human h-NUMB encod	C 958	14	2.5	4219	18	V74523	Human strmallin-2
C 886	14	2.5	2995	19	V70355	Mouse developing l	C 959	14	2.5				Staphylococcus aur
C 887	14	2.5	2995	20	V64417		C 960	14	2.5				

OY 481 CCCGAGTTATTAACCGGATTCCTCGTTTTCACATCTATATAAGACAGTATTTTAAATCA 540
 |||||||
 DB 481 ccgagttatcagcagatctcgttttaccattcataaagacagattttaatca 540
 OY 541 TACACTAAGCATAG 555
 |||||||
 DB 541 tacactaaacagatag 555

RESULT 2

T79300/C
 ID T79300 standard; cDNA; 31 BP.

AC T79300;

DT 17-FEB-1998 (first entry)

DE Staphylothermus marinus esterase Fl-12LC gene 3' PCR primer.

KW Esterase; thermostable enzyme; ester; chiral compound; cheese;

KM pulp; paper; lignin removal; sugar; lignocellulose;

KW disease resistance; feedstuff; primer; PCR; ss.

OS Synthetic.

OS Staphylothermus marinus strain F1.

PN MO9730160-A1.

PD 21-AUG-1997.

PF 11-FEB-1997; 97WO-US02039.

PR 16-FEB-1996; 96US-0602359.

PI (RECO-) RECOMBINANT BIOCATALYSIS INC.

PI Callen W, Kosmotka A, Link S, Maffia AM, Murphy D;

PI Reid J, Robertson DE, Swanson RV, Warren PV;

DR WPI; 1997-425035/39.

PT Nucleic acid encoding heat stable esterase from thermophilic

PT bacteria - which is active in organic solvents, useful in cheese or

PT paper manufacture, and to study plant resistance to disease

PS Example 1; Page 28; 113pp; English.

XX A 3' PCR primer (T79300) and a 5' PCR primer (T79299) can be used

CC to amplify the esterase Fl-12LC gene (see T79321) of

CC Staphylothermus marinus F1 from a pBluescript vector containing

CC the DNA. The amplified sequence can then be inserted into a pOET

CC vector, and the esterase (see W23069) expressed in bacterial host

CC cells. Novel esterases (see W23069-88) are provided that are

CC stable at high temperature and in organic solvents, making them

CC superior for use in production of pure chiral compounds used in

CC the pharmaceutical, agricultural and other chemical industries.

XX Sequence 31 BP; 7 A; 4 C; 7 G; 13 T; 0 other;

Query Match 3.88; Score 21; DB 18; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 535 AATCATACACTAAGCATAG 555

DB 31 AATCATACACTAAGCATAG 11

RESULT 3

T79299

ID T79299 standard; cDNA; 52 BP.

XX T79299;

AC 17-FEB-1998 (first entry)

DT Staphylothermus marinus esterase Fl-12LC gene 5' PCR primer.

KW Esterase; thermostable enzyme; ester; chiral compound; cheese;

KM pulp; paper; lignin removal; sugar; lignocellulose;

KW disease resistance; feedstuff; primer; PCR; ss.

OS Synthetic.

OS Staphylothermus marinus strain F1.

PN MO9730160-A1.

PD 21-AUG-1997.

PF 11-FEB-1997; 97WO-US02039.

PR 16-FEB-1996; 96US-0602359.

PI (RECO-) RECOMBINANT BIOCATALYSIS INC.

PI Callen W, Kosmotka A, Link S, Maffia AM, Murphy D;

PI Reid J, Robertson DE, Swanson RV, Warren PV;

DR WPI; 1997-425035/39.

PT Nucleic acid encoding heat stable esterase from thermophilic

PT bacteria - which is active in organic solvents, useful in cheese or

PT paper manufacture, and to study plant resistance to disease

PS Example 1; Page 28; 113pp; English.

XX A 5' PCR primer (T79299) and a 3' PCR primer (T79300) can be used

CC to amplify the esterase Fl-12LC gene (see T79321) of

CC Staphylothermus marinus F1 from a pBluescript vector containing

CC the DNA. The amplified sequence can then be inserted into a pOET

CC vector, and the esterase (see W23069) expressed in bacterial host

CC cells. Novel esterases (see W23069-88) are provided that are

CC stable at high temperature and in organic solvents, making them

CC superior for use in production of pure chiral compounds used in

CC the pharmaceutical, agricultural and other chemical industries.

XX Sequence 52 BP; 21 A; 9 C; 8 G; 14 T; 0 other;

Query Match 3.88; Score 21; DB 18; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCTTTTAAACAGCACTCT 21

DB 32 atgctttaacaagcactct 52

RESULT 4

V52181/C

ID V52181 standard; DNA; 25002 BP.

AC V52181;

DT 23-OCT-1998 (first entry)

DE Streptococcus pneumoniae genome fragment SEQ ID NO:48.

KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;

OS computer readable medium; vaccine; pharmaceutical composition; ds.

PN Streptococcus pneumoniae.

MO9818931-A2.

XX 07-MAY-1998.
 PD 30-OCT-1997; 97WO-US19588.
 XX 31-OCT-1996; 96US-0029960.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
 PI Kunsch CA, Rosen CA;
 XX WPI; 1998-272225/24.
 DR Computer-readable medium with recorded Streptococcus pneumoniae
 XX polynucleotide sequences - useful in diagnostic kits and assays, and
 PT pharmaceutical compositions and vaccines for Streptococcus
 PT pneumoniae
 PS Claim 1; Page 431-445; 1409pp; English.
 XX The present invention describes a computer readable medium which has
 CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
 CC on it, or a representative fragment of a sequence at least 95% identical
 CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
 CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus
 CC pneumoniae. The present invention also describes an isolated nucleic acid
 CC molecule encoding a homologue of any of the fragments of the S. pneumoniae
 CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
 CC by a process comprising: (a) screening a genomic DNA library using as a
 CC probe a target sequence defined by any of the sequences in SEQ ID NO:1
 CC to 391, identifying members of the library which contain sequences
 CC that hybridize to the target sequence and isolating the nucleic acid
 CC molecules from the members; or (b) isolating mRNA, DNA or cDNA produced
 CC from an organism, amplifying nucleic acid molecules whose nucleotide
 CC sequence is homologous to amplification primers derived from the
 CC fragment of the S. pneumoniae genome to prime the amplification and
 CC isolating the amplified sequences. The computer readable medium can be
 CC used in a computer-based system for identifying fragments of the
 CC S. pneumoniae genome of commercial importance, or expression modulating
 CC fragments of the S. pneumoniae genome. Products from the present
 CC invention can be used in diagnosis kits and assays, and pharmaceutical
 CC compositions and vaccines for S. pneumoniae.
 CC Sequence 25002 BP; 7422 A; 5498 C; 4618 G; 7463 T; 1 other;
 SQ

Query Match 3.2%; Score 18; DB 19; Length 25002;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 182 TTGCAATTGGTGGATAC 199
 ||||||||||||||||
 DB 17016 TTGCAATTGGTGGATAC 16999

RESULT 5
 X83005/c
 ID X83005 standard; DNA; 29604 BP.
 AC X83005;
 XX
 XX 31-AUG-1999 (first entry)
 XX Partial mouse WRN genomic sequence #1.
 DE
 XX Mouse; WRN; Werner's syndrome; detection; diagnosis; autosomal;
 KW recessive disorder; phenotype; ss.
 XX Mus musculus.
 OS
 XX W09724435-A1.
 XX

PD 10-JUL-1997.
 XX 30-DEC-1996; 96WO-US20785.
 XX 12-APR-1996; 96US-0632175.
 PR 29-DEC-1995; 95US-0009409.
 PR 29-DEC-1995; 95US-0580539.
 PR 30-JAN-1996; 96US-0010835.
 PR 30-JAN-1996; 96US-0594242.
 XX (DARW-) DARWIN MOLECULAR CORP.
 PA (OSHI/) OSHIMA J.
 XX Fu Y, Mulligan J, Oshima J, Schellenberg GD, Yu C;
 PI WPI; 1997-363671/33.
 DR Isolated nucleic acid molecule encoding the WRN gene product
 XX useful for detection and treatment of Werner's syndrome, and related
 PT diseases
 PT
 PS Claim 1; Fig 7; 153pp; English.
 XX This sequence represents a fragment of the genomic sequence containing
 CC the coding region for the mouse WRN gene (X83004). The corresponding
 CC human gene (X83001) encodes a protein related to Werner's syndrome.
 CC The products can be used for the detection and treatment of Werner's
 CC syndrome (WS), an autosomal recessive disorder with a complex phenotype,
 CC as well as related diseases.
 CC Sequence 29604 BP; 7634 A; 5861 C; 5985 G; 10123 T; 1 other;
 SQ

Query Match 3.2%; Score 18; DB 18; Length 29604;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 99 ATGGTTTAATATATGGA 116
 ||||||||||||||||
 DB 29176 ATGGTTTAATATATGGA 29159

RESULT 6
 X52014
 ID X52014 standard; DNA; 157 BP.
 AC X52014;
 XX
 XX 22-JUN-1999 (first entry)
 XX Human secreted protein 5' EST SEQ ID NO: 228.
 DE Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
 XX Homo sapiens.
 OS
 XX W09906552-A2.
 XX 11-FEB-1999.
 PD 31-JUL-1998; 98WO-1B01236.
 PF 01-AUG-1997; 97US-0905223.
 PR (GSEST) GENSET.
 PA
 XX Duclert A, Dumas Milne Edwards J, Lacroix B;
 XX


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XX Dumas MLine Edwards J, Duclert A, Giordano J;
XX WPI: 2000-500381/45.
XX P-PSDB: G03846.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1: SEQ ID 3850; 71bp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. An ORF has been identified within the
XX sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX derived from 30 different tissues. EST sequences usually correspond
XX mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX well suited for isolating cDNA sequences derived from the 5' ends of
XX mRNAs and even in those cases where longer cDNA sequences have been
XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX mRNAs with intact 5' ends and can therefore be used to obtain full length
XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX gene therapy and chromosome mapping procedures. They are used to obtain
XX upstream regulatory sequences and to design expression and secretion
XX vectors.
XX
XX Sequence 361 BP; 124 A; 50 C; 74 G; 113 T; 0 other:
XX
XX
XX Query Match          3.1%; Score 17; DB 21; Length 361;
XX Best Local Similarity 100.0%; Pred. No. 38;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 204 TGTATAGTTGGTTTAA 220
XX      |||||||
XX DB 247 tgtatagttggtttaa 263
XX
XX
XX RESULT 9
XX ID T26471 standard; cDNA to mRNA; 422 BP.
XX AC T26471;
XX DT 23-OCT-1996 (first entry)
XX DE Human gene signature HUMGS08713.
XX DE
XX KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
XX human; cloning; mapping; non-biased library; diagnosis; detection;
XX cell typing; abnormal cell function; ss.
XX OS Homo sapiens.
XX OS
XX PN W09514772-A1.
XX PD 01-JUN-1995.
XX PF 11-NOV-1994; 94WO-JP01916.
XX PR 12-NOV-1993; 93JP-0355504.
XX PA (MATS/) MATSUBARA K.
XX PA (OKUB/) OKUBO K.
XX PI Matsubara K, Okubo K;
XX WPI: 1995-206931/27.
XX
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
XX for diagnosis of abnormal cell function, by preparing cDNA that
XX reflects relative abundance of corresp. mRNA in specific human
XX

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PF tissues
XX Claim 1: Page 2094; 2245bp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp.
XX double-stranded DNA) which comprises one of the 7837 "GS" sequences
XX given in T19001-T26837 and which is able to hybridise to part of
XX human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
XX sequences were obtained from 3'-directed cDNA libraries prepared
XX from various human tissues; synthesis of cDNA was initiated from the
XX 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
XX untranslated sequence is unique to a particular mRNA species, almost
XX all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
XX is constructed so as to reflect accurately the relative abundance of
XX different mRNAs in the particular tissue from which it was derived.
XX The appearance frequency of a given GS in a cDNA library can be
XX determined (esp. using primers and probes derived from the GS
XX sequences) as a means of diagnosing abnormal cell function or for
XX recognising different cell types.
XX
XX Sequence 422 BP; 112 A; 70 C; 83 G; 142 T; 15 other:
XX
XX
XX Query Match          3.1%; Score 17; DB 16; Length 422;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 204 TGTATAGTTGGTTTAA 220
XX      |||||||
XX DB 138 tgtatagttggtttaa 154
XX
XX
XX RESULT 10
XX ID C35823/c standard; DNA; 486 BP.
XX AC C35823;
XX DT 17-OCT-2000 (first entry)
XX DE Zea mays DNA fragment SEQ ID NO: 11554.
XX DE
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic;
XX pathway; promoter; termination sequence; corn; ss.
XX OS Zea mays subsp. mays.
XX OS
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 23-APR-1999; 99US-0130891.
XX PR 28-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 30-APR-1999; 99US-0132407.
XX PR 04-MAY-1999; 99US-0132484.
XX PR 05-MAY-1999; 99US-0132485.
XX

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PR	06-MAY-1999;	99US-0132486;
PR	06-MAY-1999;	99US-0132487;
PR	07-MAY-1999;	99US-0132863;
PR	11-MAY-1999;	99US-0134256;
PR	14-MAY-1999;	99US-0134218;
PR	14-MAY-1999;	99US-0134219;
PR	14-MAY-1999;	99US-0134221;
PR	14-MAY-1999;	99US-0134320;
PR	18-MAY-1999;	99US-0134371;
PR	19-MAY-1999;	99US-0134941;
PR	20-MAY-1999;	99US-0135124;
PR	21-MAY-1999;	99US-0135353;
PR	24-MAY-1999;	99US-0135629;
PR	25-MAY-1999;	99US-0136021;
PR	27-MAY-1999;	99US-0136392;
PR	28-MAY-1999;	99US-0136788;
PR	01-JUN-1999;	99US-0136788;
PR	03-JUN-1999;	99US-0137528;
PR	04-JUN-1999;	99US-0137502;
PR	07-JUN-1999;	99US-0137724;
PR	08-JUN-1999;	99US-0138094;
PR	10-JUN-1999;	99US-0138540;
PR	10-JUN-1999;	99US-0138847;
PR	14-JUN-1999;	99US-0139119;
PR	16-JUN-1999;	99US-0139452;
PR	17-JUN-1999;	99US-0139453;
PR	17-JUN-1999;	99US-0139492;
PR	18-JUN-1999;	99US-0139454;
PR	18-JUN-1999;	99US-0139455;
PR	18-JUN-1999;	99US-0139456;
PR	18-JUN-1999;	99US-0139457;
PR	18-JUN-1999;	99US-0139458;
PR	18-JUN-1999;	99US-0139459;
PR	18-JUN-1999;	99US-0139460;
PR	18-JUN-1999;	99US-0139461;
PR	18-JUN-1999;	99US-0139462;
PR	18-JUN-1999;	99US-0139463;
PR	18-JUN-1999;	99US-0139750;
PR	18-JUN-1999;	99US-0139763;
PR	21-JUN-1999;	99US-0139817;
PR	22-JUN-1999;	99US-0139899;
PR	23-JUN-1999;	99US-0140353;
PR	23-JUN-1999;	99US-0140354;
PR	24-JUN-1999;	99US-0140695;
PR	28-JUN-1999;	99US-0140823;
PR	29-JUN-1999;	99US-0140991;
PR	30-JUN-1999;	99US-0141287;
PR	01-JUL-1999;	99US-0141847;
PR	01-JUL-1999;	99US-0142154;
PR	02-JUL-1999;	99US-0142055;
PR	06-JUL-1999;	99US-0142390;
PR	08-JUL-1999;	99US-0142803;
PR	09-JUL-1999;	99US-0142920;
PR	12-JUL-1999;	99US-0142927;
PR	13-JUL-1999;	99US-0143542;
PR	14-JUL-1999;	99US-0143624;
PR	15-JUL-1999;	99US-0144005;
PR	16-JUL-1999;	99US-0144085;
PR	16-JUL-1999;	99US-0144086;
PR	19-JUL-1999;	99US-0144325;
PR	19-JUL-1999;	99US-0144331;
PR	19-JUL-1999;	99US-0144332;
PR	19-JUL-1999;	99US-0144333;
PR	19-JUL-1999;	99US-0144334;
PR	19-JUL-1999;	99US-0144335;
PR	20-JUL-1999;	99US-0144352;
PR	20-JUL-1999;	99US-0144633;
PR	20-JUL-1999;	99US-0144684;
PR	21-JUL-1999;	99US-0144814;
PR	21-JUL-1999;	99US-0145086;
PR	21-JUL-1999;	99US-0145088;
PR	22-JUL-1999;	99US-0145087;
PR	22-JUL-1999;	99US-0145087;
PR	22-JUL-1999;	99US-0145089;
PR	22-JUL-1999;	99US-0145145;
PR	23-JUL-1999;	99US-0145218;
PR	23-JUL-1999;	99US-0145224;
PR	26-JUL-1999;	99US-0145276;
PR	27-JUL-1999;	99US-0145913;
PR	27-JUL-1999;	99US-0145918;
PR	27-JUL-1999;	99US-0145919;
PR	28-JUL-1999;	99US-0145951-
PR	02-AUG-1999;	99US-0145386;
PR	02-AUG-1999;	99US-0146388;
PR	02-AUG-1999;	99US-0146389;
PR	03-AUG-1999;	99US-0147038;
PR	04-AUG-1999;	99US-0147204;
PR	04-AUG-1999;	99US-0147302;
PR	05-AUG-1999;	99US-0147192;
PR	06-AUG-1999;	99US-0147260;
PR	06-AUG-1999;	99US-0147303;
PR	06-AUG-1999;	99US-0147416;
PR	09-AUG-1999;	99US-0147493;
PR	10-AUG-1999;	99US-0147935;
PR	10-AUG-1999;	99US-0148171;
PR	11-AUG-1999;	99US-0148319;
PR	12-AUG-1999;	99US-0148341;
PR	13-AUG-1999;	99US-0148565;
PR	13-AUG-1999;	99US-0148684;
PR	16-AUG-1999;	99US-0149368;
PR	17-AUG-1999;	99US-0149175;
PR	18-AUG-1999;	99US-0149426;
PR	20-AUG	

PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161932.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 3.1%; Score 17; DB 21; Length 486;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 154 ACTGTTGCTCAATATAT 170
|||||
DB 218 ACTGTTGCTCAATATAT 202

RESULT 11
C94715/c
ID C94715 standard; cDNA; 498 BP.

XX C94715;

DT 19-FEB-2001 (first entry)

XX Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1210.

XX Cat flea: hindgut and Malpighian tubule nucleic acid; HMT;

KM flea infestation; vaccine; antiparasitic; therapeutic target;

XX diagnosis; detection; ss.

OS Ctenocephalides felis.

XX WO200061621-A2.

PD 19-OCT-2000.

XX 07-APR-2000; 2000WO-US09437.

XX 09-APR-1999; 99US-0128704.

PA (HESK-) HESKA CORP.

PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

DR WPI: 2000-6556323/63.

PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic

PT acids useful for the prevention, diagnosis and treatment of flea

XX infestations -

XX Claim 26: Page 636; 964pp; English.

XX The invention relates to novel cat flea (Ctenocephalides felis) nucleic

XX acids which are expressed in hindgut and Malpighian tubule (HMT) tissue

XX or head and nerve cord (HNC) tissue. The invention also relates to the

XX encoded proteins. The invention additionally encompasses expression

XX constructs, recombinant viruses and recombinant cells comprising the

XX nucleic acids of the invention, recombinant production of the proteins,

XX antibodies against the proteins, a method of identifying inhibitors of

XX the proteins, and compositions comprising the inhibitors for

XX administration to an animal. The nucleic acids, and the proteins they

XX encode may be used in the prevention, treatment and diagnosis of diseases

XX associated with flea infestations. For example, the nucleic acids may be

XX used to produce an HMT or HNC protein according to standard recombinant

CC DNA methodology by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The HMT and HNC nucleic acids
CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
CC and quantitate the presence of cat flea or other homologous nucleic acid
CC sequences in samples. They may also be used to study the expression and
CC function of the proteins and their role in metabolism. The HMT and HNC
CC proteins may be used as antigens in the production of specific
CC antibodies, and in assays to identify modulators (agonists and
CC antagonists) of HMT and/or HNC protein expression and activity. The
CC anti-HMT/HNC protein antibodies and antigens may also be used to
CC downregulate protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of flea polypeptides
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC present sequence represents a cat flea HMT cDNA of the invention.

SO Sequence 498 BP; 179 A; 47 C; 74 G; 186 T; 12 other;

Query Match 3.1%; Score 17; DB 21; Length 498;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 276 ATTCTTACTTAAATAG 292
|||||
DB 496 ATTCTTACTTAAATAG 480

RESULT 12
Z16638/c
ID Z16638 standard; cDNA; 849 BP.

XX Z16638;

DT 12-OCT-1999 (first entry)

XX Human gene expression product cDNA sequence SEQ ID NO:4108.

XX Human; gene; gene expression product; diagnosis; therapy; probe;

KM detection; mapping; tissue typing; profiling; forensic; cancer;

XX genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.

OS Homo sapiens.

XX WO9938972-A2.

PD 05-AUG-1999.

XX 28-JAN-1999; 99WO-US01619.

XX 03-APR-1998; 98US-0080666.

PR 28-JAN-1998; 98US-0072910.

PR 24-FEB-1998; 98US-0075954.

PR 31-MAR-1998; 98US-0080114.

PR 03-APR-1998; 98US-0080515.

XX (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;

PI Escobedo J, Garcia PD, Garcia V, Gliese K, Innis MA;

PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;

PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;

PI Stache-Crain B, Sudduth-Klinger J, Williams LT;

DR WPI: 1999-494092/41.

PT Novel human genes and their expression products which are

PT differentially expressed in different cell types

XX Claim 1: Page 1947; 2479pp; English.

XX The present invention describes a library of human polynucleotides

XX comprising the sequences given in Z12532 to Z17779. Also described is a

PA (UWRO-) ROCKFELLER UNIV.
 XX
 PI Coruzzi GM, Tsai FY;
 XX
 DR WPI, 1990-361471/48.
 XX
 PT Plant asparagine synthetase - includes DNA expression system and
 XX transgenic plants
 PS
 XX Claim 33: Fig 12: 91pp; English.
 CC The promoter sequence corresponding to nucleotides 1 to 1031 is
 CC used to control expression of as2 in transgenic plants. The
 CC promoter is induced in cotyledons during germination, in nitrogen
 CC fixing root nodules and in leaves, stem and roots by dark treat-
 CC ment. The promoter and the as2 sequences can be cloned into
 CC expression vectors to produce AS2 which can be used to engineer
 CC herbicide resistance, as a dominant selectable marker, to select
 CC novel herbicides or compounds useful for synchronising plant cells
 CC in culture, etc.
 CC See also Q06598, Q06599 and Q06622.
 CC
 XX
 SQ Sequence 1121 BP: 424 A; 156 G; 150 G; 388 T; 3 other;

Query Match 3.1%; Score 17; DB 11; Length 1121;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 336 AGTATTGTTTCTTAT 352
 |||
 DB 798 AGTATTGTTTCTTAT 782

RESULT 15

A99072/c
 ID A99072 standard; DNA: 1563 BP.

AC A99072;

DT 18-JAN-2001 (first entry)

XX Arabidopsis thaliana basl nucleotide sequence SEQ ID NO:1.

KW Arabidopsis thaliana; basl; promoter; cytochrome P450; CYP72B1; plant;
 KM brassinosteroid signalling; brassinosteroid synthesis; brassinolide; ds.

OS Arabidopsis thaliana.

OS WO200055302-A2.

PD 21-SEP-2000.

PF 16-MAR-2000; 2000WO-US06915.

PR 16-MAR-1999; 99US-0124570.

PR 14-DEC-1999; 99US-0170931.

PR 20-DEC-1999; 99US-0172832.

PA (SALK) SALK INST BIOLOGICAL STUDIES.

PI Neff MM, Chory J;

DR WPI, 2000-638195/61.

DR P-PSDB; B23917.

XX Transgenic plants having modulated brassinolide synthesis resulting in
 PT insect resistance, dwarfism and darker-green foliage compared with
 PT wild-type plants; have nucleic acid encoding Basl polypeptide in its
 PT genome

PS Disclosure: Fig 1A; 104pp; English.

CC The present invention describes a genetically modified plant (I)
 CC comprising at least one exogenous nucleic acid sequence encoding a Basl
 CC polypeptide, homologue or functional fragment, in its genome or at least
 CC one regulatory sequence that modified expression of endogenous basl
 CC gene, homologue or functional fragment, and which is characterised as
 CC having modulated brassinolide activity or synthesis. The basl gene
 CC encodes a cytochrome P450 (CYP72B1), which has a role in brassinosteroid
 CC signalling or synthesis. Overexpression of the basl gene in plants
 CC causes a dark green, dwarf phenotype which mimics plants that have low
 CC levels of the plant hormone, brassinolide. Overexpression of the basl
 CC gene also increases resistance to insects in plants. The present
 CC sequence represents the Arabidopsis basl nucleotide sequence, which is
 CC used in the exemplification of the present invention.

SQ Sequence 1563 BP: 424 A; 310 G; 377 G; 452 T; 0 other;

Query Match 3.1%; Score 17; DB 21; Length 1563;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 AGCTGTTCTACTAATTA 418
 |||
 DB 648 AGCTGTTCTACTAATTA 632

Search completed: May 31, 2001, 02:17:19
 Job time: 4480 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2001, 01:01:09 ; Search time 63.31 Seconds
(without alignments)
1530.635 Million cell updates/sec

Title: US-09-382-242-23

Perfect score: 555

Sequence: 1 ATGCTTTAAACAGACACTC.....AATCATACCTAAACGATAG 555

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 302621 seqs, 87301344 residues

Word size: 0

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

Issued_Patents_NA:*
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2: /cgnl_7/prodata/1/lna/5B_COMB.seq:*
3: /cgnl_7/prodata/1/lna/5A_COMB.seq:*
4: /cgnl_7/prodata/1/lna/5B_COMB.seq:*
5: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:*
6: /cgnl_7/prodata/1/lna/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	555	2	US-08-602-359A-23
2	21	3.8	31	2	US-08-602-359A-2
3	21	3.8	52	2	US-08-602-359A-1
4	18	3.2	29604	3	US-08-781-891-207
5	17	3.1	1121	6	5256558-7
6	16	2.9	837	3	US-08-549-515-4
7	16	2.9	1700	2	US-08-897-340-4
8	16	2.9	1700	4	US-09-252-329-4
9	16	2.9	2483	1	US-08-464-340A-3
10	16	2.9	2483	5	PCT-US94-08449A-3
11	16	2.9	3386	1	US-08-703-809-2
12	16	2.9	3386	1	US-08-703-809-2
13	16	2.9	3386	2	US-08-014-066-2
14	16	2.9	3386	2	US-08-703-807-2
15	16	2.9	3386	2	US-09-211-631-2
16	16	2.9	3386	4	US-09-265-628-2
17	16	2.9	3386	4	US-09-001-141-2
18	16	2.9	3386	4	US-08-549-515-1
19	16	2.9	4051	3	US-08-322-962-3
20	15	2.7	580	1	US-08-450-653-3
21	15	2.7	1016	2	US-08-930-617-1
22	15	2.7	1178	2	US-08-933-750C-38
23	15	2.7	1178	4	US-09-234-613-88
24	15	2.7	1203	3	US-09-122-443-3
25	15	2.7	1419	2	US-08-194-981E-4
26	15	2.7	1591	2	US-08-194-981E-3
27	15	2.7	1591	2	US-08-194-981E-3

28	15	2.7	1641	1	US-08-385-229-1	Sequence 1, App1
29	15	2.7	1641	2	US-08-650-000-1	Sequence 1, App1
30	15	2.7	1641	6	5395760-1	Patent No. 5395760
31	15	2.7	1852	1	US-08-201-118-10	Sequence 10, App1
32	15	2.7	1852	2	US-08-238-821B-10	Sequence 10, App1
33	15	2.7	1852	5	PCT-US95-05744-10	Sequence 10, App1
34	15	2.7	1854	1	US-08-201-118-4	Sequence 4, App1
35	15	2.7	1854	2	US-08-238-821B-4	Sequence 4, App1
36	15	2.7	1854	5	PCT-US95-05744-4	Sequence 4, App1
37	15	2.7	2265	2	US-08-940-332-1	Sequence 2, App1
38	15	2.7	2684	2	US-08-984-171-2	Sequence 2, App1
39	15	2.7	2957	2	US-08-394-152A-48	Sequence 39, App1
40	15	2.7	3017	2	US-08-394-152A-39	Sequence 39, App1
41	15	2.7	3030	2	US-08-680-326-24	Sequence 24, App1
42	15	2.7	3509	1	US-08-322-962-1	Sequence 1, App1
43	15	2.7	3509	2	US-08-450-653-1	Sequence 1, App1
44	15	2.7	3567	2	US-08-658-665-69	Sequence 69, App1
45	15	2.7	3567	4	US-08-796-101-33	Sequence 69, App1
46	15	2.7	3655	4	US-08-878-474-6	Sequence 63, App1
47	15	2.7	4075	2	US-08-658-665-67	Sequence 67, App1
48	15	2.7	4075	2	US-08-796-101-31	Sequence 31, App1
49	15	2.7	4909	2	US-08-658-665-68	Sequence 68, App1
50	15	2.7	4909	4	US-08-796-101-32	Sequence 32, App1
51	15	2.7	6749	2	US-08-658-665-171	Sequence 71, App1
52	15	2.7	6749	2	US-08-658-665-177	Sequence 177, App1
53	15	2.7	6749	4	US-08-796-101-35	Sequence 35, App1
54	15	2.7	6749	4	US-08-796-101-38	Sequence 38, App1
55	15	2.7	40138	4	US-09-090-793-12	Sequence 12, App1
56	15	2.7	40352	2	US-08-846-111D-15	Sequence 15, App1
57	15	2.7	66516	2	US-08-996-306-1	Sequence 1, App1
58	15	2.7	246240	2	US-08-724-394A-20	Sequence 20, App1
59	15	2.7	246240	2	US-08-724-394A-20	Sequence 20, App1
60	15	2.7	246240	2	US-08-724-394A-21	Sequence 21, App1
61	15	2.7	246240	2	US-08-724-394A-21	Sequence 21, App1
62	15	2.7	246240	2	US-08-724-394A-22	Sequence 22, App1
63	15	2.7	246240	2	US-08-724-394A-22	Sequence 22, App1
64	15	2.5	18	3	US-08-467-023-17	Sequence 17, App1
65	14	2.5	24	3	US-08-193-627-30	Sequence 30, App1
66	14	2.5	38	1	US-08-259-612A-2	Sequence 2, App1
67	14	2.5	38	1	US-08-644-291-2	Sequence 2, App1
68	14	2.5	46	2	US-08-658-665-115	Sequence 115, App1
69	14	2.5	46	4	US-08-796-101-91	Sequence 91, App1
70	14	2.5	54	4	US-08-658-665-118	Sequence 118, App1
71	14	2.5	54	4	US-08-796-101-94	Sequence 94, App1
72	14	2.5	55	1	US-08-323-084A-18	Sequence 18, App1
73	14	2.5	55	1	US-08-674-008-18	Sequence 18, App1
74	14	2.5	66	2	US-08-566-398-8	Sequence 8, App1
75	14	2.5	92	2	US-08-566-398-4	Sequence 376, App1
76	14	2.5	95	1	US-08-105-483-376	Sequence 376, App1
77	14	2.5	95	1	US-08-709-209-376	Sequence 376, App1
78	14	2.5	95	1	US-08-458-101-376	Sequence 167, App1
79	14	2.5	99	2	US-08-658-665-167	Sequence 167, App1
80	14	2.5	99	4	US-08-796-101-143	Sequence 143, App1
81	14	2.5	104	1	US-07-745-206A-4	Sequence 4, App1
82	14	2.5	104	1	US-08-455-043A-2	Sequence 2, App1
83	14	2.5	104	2	US-08-193-078B-2	Sequence 2, App1
84	14	2.5	104	2	US-08-223-305C-2	Sequence 2, App1
85	14	2.5	104	2	US-08-149-097D-2	Sequence 2, App1
86	14	2.5	104	2	US-08-311-363-4	Sequence 4, App1
87	14	2.5	104	3	US-08-949-386-2	Sequence 2, App1
88	14	2.5	104	3	US-08-450-662-2	Sequence 2, App1
89	14	2.5	107	1	US-08-105-483-435	Sequence 435, App1
90	14	2.5	107	1	US-08-709-209-435	Sequence 435, App1
91	14	2.5	107	1	US-08-303-275-143	Sequence 143, App1
92	14	2.5	107	1	US-08-458-101-435	Sequence 143, App1
93	14	2.5	110	6	5174993-18	Patent No. 5174993
94	14	2.5	110	6	5505941-18	Patent No. 5505941
95	14	2.5	135	5	US-08-611-757-21	Sequence 21, App1
96	14	2.5	135	5	PCT-US95-05980-21	Sequence 21, App1
97	14	2.5	342	5	PCT-US97-09955-14	Sequence 14, App1
98	14	2.5	363	1	US-08-040-204-8	Sequence 8, App1
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100	14	2.5	400	3	US-09-265-315-4	Sequence 4, App1

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C 104	14	2.5	583	4	US-09-404-671-5	177	14	2.5	1749	1	US-08-116-098-1
C 105	14	2.5	583	4	US-09-404-671-7	178	14	2.5	1821	4	US-08-845-256-6
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C 108	14	2.5	786	2	US-08-989-478-15	181	14	2.5	1975	6	5436393-1
C 109	14	2.5	786	3	US-08-996-685-15	182	14	2.5	1986	2	US-08-528-057-43
C 110	14	2.5	786	5	PCT-US93-10034-3	183	14	2.5	1992	1	US-08-485-288A-3
C 111	14	2.5	809	4	US-09-276-531-27	184	14	2.5	2001	3	US-08-714-918-92
C 112	14	2.5	840	1	US-07-940-605A-1	185	14	2.5	2001	4	US-09-265-315-92
C 113	14	2.5	840	1	US-08-184-422-7	186	14	2.5	2001	4	US-09-265-315-92
C 114	14	2.5	840	1	US-08-360-923A-1	187	14	2.5	2011	2	US-08-989-478-6
C 115	14	2.5	840	1	US-08-431-055-3	188	14	2.5	2011	2	US-08-989-478-6
C 116	14	2.5	840	2	US-08-690-096-1	189	14	2.5	2011	3	US-08-996-685-6
C 117	14	2.5	840	2	US-08-249-189-11	190	14	2.5	2011	3	US-08-996-685-6
C 118	14	2.5	840	2	US-08-484-624A-11	191	14	2.5	2071	4	US-09-023-023-1
C 119	14	2.5	840	3	US-08-477-733B-11	192	14	2.5	2116	3	US-08-860-091A-1
C 120	14	2.5	840	3	US-08-763-995-1	193	14	2.5	2124	1	US-08-087-007-1
C 121	14	2.5	840	3	US-09-088-913A-11	194	14	2.5	2124	4	US-08-483-433-1
C 122	14	2.5	840	4	US-08-589-771B-7	195	14	2.5	2124	5	PCT-US92-05920-1
C 123	14	2.5	900	3	US-09-064-703-8	196	14	2.5	2144	2	US-08-525-742-9
C 124	14	2.5	915	3	US-09-064-703-9	197	14	2.5	2173	1	US-08-036-210-6
C 125	14	2.5	930	2	US-08-394-152A-47	198	14	2.5	2173	1	US-08-449-609-6
C 126	14	2.5	1017	3	US-08-913-842-14	199	14	2.5	2220	6	5171850-1
C 127	14	2.5	1018	6	5187262-7	200	14	2.5	2259	1	US-07-828-700-7
C 128	14	2.5	1035	2	US-08-417-210A-111	201	14	2.5	2276	3	US-08-946-026-11
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C 130	14	2.5	1070	1	US-08-441-597-1	203	14	2.5	2307	2	US-08-592-541-28
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C 135	14	2.5	1173	2	US-08-184-009-214	208	14	2.5	2309	2	US-08-449-609-10
C 136	14	2.5	1173	2	US-08-458-356-214	209	14	2.5	2441	1	US-08-920-812-12
C 137	14	2.5	1173	4	US-08-796-101-45	210	14	2.5	2441	1	US-08-920-812-12
C 138	14	2.5	1194	2	US-08-989-478-13	211	14	2.5	2441	1	US-08-921-177-12
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C 140	14	2.5	1235	6	5171685-1	213	14	2.5	2441	2	US-08-362-577C-12
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C 142	14	2.5	1305	1	US-08-185-851A-1	215	14	2.5	2539	2	US-08-432-016-1
C 143	14	2.5	1337	3	US-08-467-023-1	216	14	2.5	2539	2	US-08-684-594-1
C 144	14	2.5	1349	2	US-08-676-782-10	217	14	2.5	2559	3	US-09-070-060-2
C 145	14	2.5	1353	2	US-08-611-280-1	218	14	2.5	2559	3	US-09-357-746-2
C 146	14	2.5	1368	2	US-08-204-288-1	219	14	2.5	2651	2	US-08-631-607-1
C 147	14	2.5	1387	2	US-08-525-742-3	220	14	2.5	2651	4	US-08-658-665-49
C 148	14	2.5	1505	2	US-08-909-965C-13	221	14	2.5	2692	1	US-08-796-101-13
C 149	14	2.5	1529	1	US-08-448-110-1	222	14	2.5	2692	2	US-08-036-210-14
C 150	14	2.5	1529	6	5436393-2	223	14	2.5	2780	1	US-08-449-609-14
C 151	14	2.5	1530	1	US-08-458-084-3	224	14	2.5	2852	3	US-08-441-139-1
C 152	14	2.5	1530	2	US-08-205-508-3	225	14	2.5	2852	3	US-09-027-137-2
C 153	14	2.5	1530	2	US-08-482-148-8	226	14	2.5	2989	2	US-08-458-434A-4
C 154	14	2.5	1530	5	PCT-US95-02944-8	227	14	2.5	2989	2	US-08-565-398-9
C 155	14	2.5	1530	5	PCT-US95-02945-3	228	14	2.5	3058	4	US-08-841-349-12
C 156	14	2.5	1533	1	US-08-483-223-23	229	14	2.5	3065	4	US-09-276-531-107
C 157	14	2.5	1533	2	US-08-485-938A-23	230	14	2.5	3097	2	US-08-209-521-28
C 158	14	2.5	1533	3	US-08-910-041-23	231	14	2.5	3288	1	US-08-849-480A-2
C 159	14	2.5	1533	3	US-09-328-474-23	232	14	2.5	3350	3	US-08-208-008C-3
C 160	14	2.5	1533	3	US-09-100-546-23	233	14	2.5	3355	2	US-09-110-116-2
C 161	14	2.5	1533	4	US-09-010-715-23	234	14	2.5	3355	2	US-08-933-821-3
C 162	14	2.5	1533	4	US-09-577-756-23	235	14	2.5	3411	2	US-08-960-507-3
C 163	14	2.5	1546	6	5514787-1	236	14	2.5	3539	1	US-08-849-480A-1
C 164	14	2.5	1567	4	US-09-276-531-75	237	14	2.5	3539	1	US-08-658-665-47
C 165	14	2.5	1590	3	US-09-064-703-1	238	14	2.5	3561	4	US-08-796-101-11
C 166	14	2.5	1597	2	US-08-989-478-9	239	14	2.5	3561	1	US-08-485-568A-3
C 167	14	2.5	1597	3	US-08-996-685-9	240	14	2.5	3561	2	US-08-357-658-5
C 168	14	2.5	1605	3	US-09-064-703-5	241	14	2.5	3561	2	US-08-590-554A-3
C 169	14	2.5	1608	2	US-08-989-478-11	242	14	2.5	3561	5	US-09-184-223-3
C 170	14	2.5	1608	2	US-08-996-685-11	243	14	2.5	3592	3	PCT-US93-12682-5
C 171	14	2.5	1610	2	US-08-540-804-17	244	14	2.5	3592	4	US-08-714-918-63
C 172	14	2.5	1610	2	US-08-218-265-17	245	14	2.5	3592	4	US-09-265-315-63
C 173	14	2.5	1610	3	US-08-521-872-17	246	14	2.5	3891	1	US-08-480-604A-27

Sequence 2, Appl	174	14	2.5	1629	1	US-08-589-080-2
Sequence 1, Appl	175	14	2.5	1659	2	US-08-528-057-1
Sequence 4, Appl	176	14	2.5	1701	3	US-09-064-703-4
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Sequence 6, Appl	178	14	2.5	1821	4	US-08-845-256-6
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Sequence 1, Appl	181	14	2.5	1975	6	5436393-1
Sequence 43, Appl	182	14	2.5	1986	2	US-08-528-057-43
Sequence 3, Appl	183	14	2.5	1992	1	US-08-485-288A-3
Sequence 92, App	184	14	2.5	2001	3	US-08-714-918-92
Sequence 92, App	185	14	2.5	2001	4	US-08-714-918-92
Sequence 92, App	186	14	2.5	2001	4	US-08-714-918-92
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Sequence 1, Appl	195	14	2.5	2124	5	PCT-US92-05920-1
Sequence 9, Appl	196	14	2.5	2144	2	US-08-525-742-9
Sequence 9, Appl	197	14	2.5	2173	1	US-08-036-210-6
Sequence 14, Appl	198	14	2.5	2173	1	US-08-449-609-6
Sequence 11, App	199	14	2.5	2220	6	5171850-1
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Sequence 1, Appl	206	14	2.5	2307	4	US-08-496-841C-8
Sequence 5, Appl	207	14	2.5	2309	2	US-08-036-210-10
Sequence 214, App	208	14	2.5	2309	2	US-08-449-609-10
Sequence 45, Appl	209	14	2.5	2441	1	US-08-920-812-12
Sequence 13, Appl	210	14	2.5	2441	1	US-08-920-812-12
Sequence 13, Appl	211	14	2.5	2441	1	US-08-921-177-12
Sequence 13, Appl	212	14	2.5	2441	1	US-08-921-177-12
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C 247	14	2.5	3891	2	US-08-405-496A-27	Sequence 27, Appl	C 320	13	2.3	20	1	US-08-409-442A-348	Sequence 348, App
C 248	14	2.5	3973	1	US-08-036-210-21	Sequence 21, Appl	C 321	13	2.3	20	2	US-08-469-609A-348	Sequence 348, App
C 249	14	2.5	3973	2	US-08-449-609-21	Sequence 21, Appl	C 322	13	2.3	20	3	US-09-289-267-59	Sequence 59, Appl
C 250	14	2.5	4071	4	US-09-091-117-3	Sequence 3, Appl1	C 323	13	2.3	20	4	US-09-143-190-348	Sequence 348, App
C 251	14	2.5	4144	1	US-08-218-686-1	Sequence 1, Appl1	C 324	13	2.3	20	4	US-09-359-756-45	Sequence 45, Appl
C 252	14	2.5	4144	3	US-08-460-242-1	Sequence 1, Appl1	C 325	13	2.3	22	4	US-08-882-046-91	Sequence 91, Appl
C 253	14	2.5	4184	2	US-08-785-310A-4	Sequence 4, Appl1	C 326	13	2.3	23	1	US-07-110-882-9	Sequence 9, Appl1
C 254	14	2.5	4319	2	PCT-US95-10661A-1	Sequence 1, Appl1	C 327	13	2.3	23	1	US-07-925-732-9	Sequence 9, Appl1
C 255	14	2.5	4427	2	US-08-658-665-48	Sequence 48, Appl	C 328	13	2.3	25	1	US-08-316-293-21	Sequence 21, Appl
C 256	14	2.5	4427	4	US-08-796-101-12	Sequence 12, Appl	C 329	13	2.3	25	1	US-08-071-601-14	Sequence 14, Appl
C 257	14	2.5	4450	4	US-08-612-8608-2	Sequence 2, Appl1	C 330	13	2.3	25	2	US-08-621-100-14	Sequence 14, Appl
C 258	14	2.5	4838	4	US-08-852-629-15	Sequence 15, Appl	C 331	13	2.3	25	4	US-09-047-347-6	Sequence 6, Appl1
C 259	14	2.5	4883	2	US-08-658-665-70	Sequence 70, Appl	C 332	13	2.3	30	1	US-08-073-799C-5	Sequence 5, Appl1
C 260	14	2.5	4883	4	US-08-796-101-34	Sequence 34, Appl	C 333	13	2.3	30	1	US-07-946-232-5	Sequence 5, Appl1
C 261	14	2.5	4972	4	US-09-035-648-17	Sequence 17, Appl	C 334	13	2.3	30	1	US-07-947-672-5	Sequence 5, Appl1
C 262	14	2.5	5062	2	US-08-658-665-187	Sequence 187, App	C 335	13	2.3	30	1	US-08-432-043-5	Sequence 5, Appl1
C 263	14	2.5	5062	4	US-08-796-101-42	Sequence 42, Appl	C 336	13	2.3	30	2	US-08-660-963-5	Sequence 5, Appl1
C 264	14	2.5	5173	1	US-08-242-677-1	Sequence 1, Appl1	C 337	13	2.3	30	2	US-08-629-001A-14	Sequence 14, Appl
C 265	14	2.5	5194	2	US-08-642-846-1	Sequence 1, Appl1	C 338	13	2.3	30	4	US-08-642-274D-220	Sequence 220, App
C 266	14	2.5	5224	2	US-08-874-186-46	Sequence 46, Appl	C 339	13	2.3	33	2	US-08-381-691-4	Sequence 4, Appl1
C 267	14	2.5	5329	2	US-09-070-060-1	Sequence 1, Appl1	C 340	13	2.3	34	2	US-08-793-410-15	Sequence 15, Appl1
C 268	14	2.5	5372	2	US-09-357-746-1	Sequence 1, Appl1	C 341	13	2.3	44	6	5464756-29	Patent No. 5464756
C 269	14	2.5	5390	5	PCT-US96-12545-5	Sequence 5, Appl1	C 342	13	2.3	48	1	US-07-977-434-37	Sequence 37, Appl
C 270	14	2.5	5421	1	US-08-118-441-28	Sequence 28, Appl	C 343	13	2.3	48	1	US-08-458-819-37	Sequence 37, Appl
C 271	14	2.5	5421	3	US-08-338-579A-28	Sequence 28, Appl	C 344	13	2.3	48	5	PCT-US91-07035-37	Sequence 37, Appl
C 272	14	2.5	5421	3	PCT-US94-09851-28	Sequence 28, Appl	C 345	13	2.3	50	6	5240845-45	Patent No. 5240845
C 273	14	2.5	5529	3	US-08-869-696-1	Sequence 1, Appl1	C 346	13	2.3	51	1	US-08-409-442A-345	Sequence 345, App
C 274	14	2.5	5590	4	US-09-050-159-129	Sequence 129, App	C 347	13	2.3	51	2	US-08-469-609A-345	Sequence 345, App
C 275	14	2.5	5622	4	US-09-067-800-3	Sequence 3, Appl1	C 348	13	2.3	51	4	US-09-143-190-345	Sequence 345, App
C 276	14	2.5	5655	2	US-08-989-478-1	Sequence 1, Appl1	C 349	13	2.3	52	6	5240845-52	Patent No. 5240845
C 277	14	2.5	5655	3	US-08-996-685-1	Sequence 1, Appl1	C 350	13	2.3	98	1	US-07-710-882-12	Sequence 12, Appl
C 278	14	2.5	5655	3	US-08-880-179-2	Sequence 2, Appl1	C 351	13	2.3	98	1	US-07-925-732-12	Sequence 12, Appl
C 279	14	2.5	5715	4	US-09-107-847-1	Sequence 1, Appl1	C 352	13	2.3	98	1	US-07-925-732-13	Sequence 13, Appl
C 280	14	2.5	6169	2	US-08-875-154-2	Sequence 2, Appl1	C 353	13	2.3	98	1	US-08-418-085-8	Sequence 8, Appl1
C 281	14	2.5	6669	4	US-09-212-971-5	Sequence 5, Appl1	C 354	13	2.3	108	2	US-09-099-011A-8	Sequence 8, Appl1
C 282	14	2.5	6702	4	US-08-800-929A-5	Sequence 5, Appl1	C 355	13	2.3	108	4	US-08-454-557C-96	Sequence 96, Appl1
C 283	14	2.5	6702	4	US-08-867-439-2	Sequence 2, Appl1	C 356	13	2.3	132	2	US-08-340-426C-96	Sequence 96, Appl1
C 284	14	2.5	6909	2	US-08-804-196-1	Sequence 1, Appl1	C 357	13	2.3	132	2	US-08-450-673C-96	Sequence 96, Appl1
C 285	14	2.5	6909	2	US-08-658-340-1	Sequence 1, Appl1	C 358	13	2.3	132	2	PCT-US95-17111A-96	Sequence 96, Appl1
C 286	14	2.5	6909	4	US-08-746-111-26	Sequence 26, Appl	C 359	13	2.3	132	3	PCT-US93-06251-31	Patent No. 5298404
C 287	14	2.5	7091	4	US-08-975-762-46	Sequence 46, Appl	C 360	13	2.3	139	5	PCT-US93-06251-31	Sequence 31, Appl1
C 288	14	2.5	7486	4	US-08-475-886-5	Sequence 5, Appl1	C 361	13	2.3	199	5	US-08-463-213-1	Sequence 1, Appl1
C 289	14	2.5	7486	4	US-08-397-232-3	Sequence 3, Appl1	C 362	13	2.3	219	6	5453566-1	Patent No. 5453566
C 290	14	2.5	7488	4	US-08-475-886-3	Sequence 3, Appl1	C 363	13	2.3	219	6	PCT-US95-10904-64	Sequence 64, Appl
C 291	14	2.5	7493	4	US-08-475-886-1	Sequence 1, Appl1	C 364	13	2.3	240	5	US-08-687-080-67	Sequence 67, Appl
C 292	14	2.5	7493	4	US-08-397-232-1	Sequence 1, Appl1	C 365	13	2.3	240	5	US-08-822-028-58	Sequence 58, Appl
C 293	14	2.5	7573	1	US-08-287-959-2	Sequence 2, Appl1	C 366	13	2.3	248	2	US-08-479-285-58	Sequence 58, Appl
C 294	14	2.5	7635	1	US-08-455-543A-23	Sequence 23, Appl	C 367	13	2.3	248	4	US-08-307-499-52	Sequence 52, Appl
C 295	14	2.5	7635	2	US-08-193-0788-29	Sequence 29, Appl	C 368	13	2.3	279	1	US-08-328-256-1	Sequence 1, Appl1
C 296	14	2.5	7635	2	US-08-223-305C-23	Sequence 23, Appl	C 369	13	2.3	360	1	US-08-820-170A-2	Sequence 2, Appl1
C 297	14	2.5	8920	2	US-08-446-855A-1	Sequence 1, Appl1	C 370	13	2.3	366	3	US-09-055-699-2	Sequence 3, Appl1
C 298	14	2.5	8920	4	US-09-150-741-1	Sequence 1, Appl1	C 371	13	2.3	366	3	US-09-273-565-2	Sequence 2, Appl1
C 299	14	2.5	9100	2	US-08-743-637B-27	Sequence 27, Appl	C 372	13	2.3	366	4	US-08-692-787-45	Sequence 45, Appl1
C 300	14	2.5	9100	3	US-08-526-840B-27	Sequence 27, Appl	C 373	13	2.3	366	4	PCT-US94-04208-5	Sequence 5, Appl1
C 301	14	2.5	9606	1	US-07-741-940-1	Sequence 1, Appl1	C 374	13	2.3	378	5	US-09-040-984-42	Sequence 42, Appl
C 302	14	2.5	9606	1	US-08-289-548A-1	Sequence 1, Appl1	C 375	13	2.3	389	4	US-08-496-841C-46	Sequence 46, Appl
C 303	14	2.5	9606	1	US-08-452-654-1	Sequence 1, Appl1	C 376	13	2.3	400	4	PCT-US94-04208-3	Sequence 3, Appl1
C 304	14	2.5	9606	2	US-08-370-235A-1	Sequence 1, Appl1	C 377	13	2.3	400	4	PCT-US96-07329-1	Sequence 1, Appl1
C 305	14	2.5	9919	3	US-08-880-179-1	Sequence 1, Appl1	C 378	13	2.3	400	2	US-08-967-101-46	Sequence 46, Appl
C 306	14	2.5	10216	2	US-08-875-154-1	Sequence 1, Appl1	C 379	13	2.3	400	2	US-08-592-541-46	Sequence 46, Appl
C 307	14	2.5	10409	3	US-08-772-440-33	Sequence 33, Appl	C 380	13	2.3	400	4	US-09-124-698-46	Sequence 46, Appl
C 308	14	2.5	10917	2	US-08-926-842B-11	Sequence 11, Appl	C 381	13	2.3	400	4	US-09-127-490-46	Sequence 46, Appl
C 309	14	2.5	12537	2	US-08-611-280-4	Sequence 4, Appl1	C 382	13	2.3	404	5	US-08-532-590-36	Sequence 36, Appl
C 310	14	2.5	12687	3	US-08-676-169-1	Sequence 1, Appl1	C 383	13	2.3	404	5	US-08-717-294-36	Sequence 36, Appl
C 311	14	2.5	12687	3	US-08-681-459-1	Sequence 1, Appl1	C 384	13	2.3	404	5	PCT-US96-07329-1	Sequence 3, Appl1
C 312	14	2.5	14855	2	US-08-687-080-59	Sequence 59, Appl	C 385	13	2.3	404	5	PCT-US93-01676A-5	Sequence 5, Appl1
C 313	14	2.5	15144	3	US-08-458-434A-6	Sequence 6, Appl1	C 386	13	2.3	404	5	US-08-324-243-36	Sequence 36, Appl
C 314	14	2.5	16442	3	US-08-781-891-208	Sequence 208, Appl	C 387	13	2.3	404	5	US-08-532-590-36	Sequence 36, Appl
C 315	14	2.5	35100	2	US-08-770-379-17	Sequence 17, Appl	C 388	13	2.3	404	5	US-08-717-294-36	Sequence 36, Appl
C 316	14	2.5	35100	4	US-08-757-669A-17	Sequence 17, Appl	C 389	13	2.3	404	5	PCT-US95-11511-36	Sequence 36, Appl
C 317	14	2.5	51952	4	US-08-947-823-1	Sequence 1, Appl1	C 390	13	2.3	405	6	5464756-17	Patent No. 5464756
C 318	14	2.5	87350	4	US-08-781-891-79	Sequence 79, Appl	C 391	13	2.3	506	1	5464756-19	Patent No. 5464756
C 319	13	2.3	18	2	US-09-156-424-36	Sequence 36, Appl	C 392	13	2.3	506	1	US-08-111-516-1	Sequence 1, Appl1

C 393	13	2.3	506	1	US-08-468-405-1	Sequence 1, Appl1	466	13	2.3	982	4	US-08-479-285-1	Sequence 1, Appl1
394	13	2.3	537	5	PCT-US95-10904-70	Sequence 70, Appl1	C 467	13	2.3	992	2	US-08-374-843B-9	Sequence 9, Appl1
395	13	2.3	540	1	US-08-117-080-15	Sequence 15, Appl1	C 468	13	2.3	992	1	US-08-905-420-9	Sequence 9, Appl1
C 396	13	2.3	543	1	US-07-912-900-25	Sequence 25, Appl1	C 469	13	2.3	993	1	US-08-364-081-2	Sequence 2, Appl1
C 398	13	2.3	543	1	US-08-285-309-25	Sequence 25, Appl1	C 470	13	2.3	993	1	US-08-630-551-2	Sequence 2, Appl1
C 399	13	2.3	543	2	US-08-502-046-25	Sequence 25, Appl1	C 471	13	2.3	993	5	PCT-US95-16558-2	Sequence 2, Appl1
C 400	13	2.3	547	1	US-08-313-075A-31	Sequence 31, Appl1	C 472	13	2.3	997	1	US-08-374-843B-16	Sequence 16, Appl1
401	13	2.3	570	1	US-08-469-667-13	Sequence 13, Appl1	C 473	13	2.3	997	2	US-08-905-420-16	Sequence 16, Appl1
402	13	2.3	570	5	PCT-US95-07289-13	Sequence 13, Appl1	C 474	13	2.3	1001	2	US-08-982-955-2	Sequence 2, Appl1
403	13	2.3	573	1	US-08-319-590-24	Sequence 24, Appl1	C 475	13	2.3	1001	4	US-09-228-311-2	Sequence 2, Appl1
404	13	2.3	573	2	US-08-487-001A-24	Sequence 24, Appl1	C 476	13	2.3	1006	5	PCT-US94-04208-8	Sequence 8, Appl1
405	13	2.3	573	2	US-08-711-905-24	Sequence 24, Appl1	C 477	13	2.3	1011	1	US-08-332-312-3	Sequence 3, Appl1
406	13	2.3	573	2	US-09-005-069-24	Sequence 24, Appl1	C 478	13	2.3	1022	1	US-08-960-780-33	Sequence 33, Appl1
407	13	2.3	591	2	US-08-487-001A-34	Sequence 34, Appl1	C 479	13	2.3	1025	3	US-08-480-640A-224	Sequence 224, App
408	13	2.3	591	2	US-08-630-822A-34	Sequence 34, Appl1	C 480	13	2.3	1025	3	US-08-480-640A-224	Sequence 224, App
409	13	2.3	591	2	US-09-005-069-34	Sequence 34, Appl1	C 481	13	2.3	1062	2	US-08-671-978A-1	Sequence 1, Appl1
410	13	2.3	600	6	5198542-12	Patent No. 5198542	C 482	13	2.3	1062	6	5395759-1	Patent No. 5395759
411	13	2.3	601	3	US-09-080-855-34	Sequence 34, Appl1	C 483	13	2.3	1070	4	US-09-118-442-16	Sequence 16, Appl1
412	13	2.3	619	3	US-08-714-918-98	Sequence 98, Appl1	C 484	13	2.3	1074	2	US-09-156-428-1	Sequence 1, Appl1
413	13	2.3	619	4	US-09-265-315-98	Sequence 98, Appl1	C 485	13	2.3	1079	1	US-08-454-196-16	Sequence 16, Appl1
414	13	2.3	619	4	US-09-265-315-98	Sequence 98, Appl1	C 486	13	2.3	1079	3	US-09-064-033-16	Sequence 16, Appl1
415	13	2.3	648	2	US-08-935-396-9	Sequence 9, Appl1	C 487	13	2.3	1082	4	US-09-118-442-28	Sequence 28, Appl1
416	13	2.3	660	3	US-09-413-452-6	Sequence 6, Appl1	C 488	13	2.3	1083	4	US-09-276-531-30	Sequence 30, Appl1
417	13	2.3	667	3	US-08-845-546-9	Sequence 9, Appl1	C 489	13	2.3	1097	4	US-09-094-103-5	Sequence 5, Appl1
C 418	13	2.3	669	4	US-09-276-531-125	Sequence 125, Appl1	C 490	13	2.3	1100	2	US-08-179-551-20	Sequence 20, Appl1
C 419	13	2.3	693	4	US-08-617-860B-11	Sequence 11, Appl1	C 491	13	2.3	1112	1	US-08-136-743B-1	Sequence 1, Appl1
C 420	13	2.3	701	3	US-08-331-625A-55	Sequence 55, Appl1	C 492	13	2.3	1116	3	US-08-918-249-3	Sequence 3, Appl1
C 421	13	2.3	730	1	US-08-036-555B-147	Sequence 147, App	C 493	13	2.3	1116	3	US-09-345-603-3	Sequence 3, Appl1
C 422	13	2.3	730	1	US-08-469-569-147	Sequence 147, App	C 494	13	2.3	1119	4	US-08-918-249-1	Sequence 1, Appl1
C 423	13	2.3	730	1	US-08-249-322A-147	Sequence 147, App	C 495	13	2.3	1119	4	US-08-345-603-1	Sequence 1, Appl1
C 424	13	2.3	730	1	US-08-469-569-147	Sequence 147, App	C 496	13	2.3	1120	4	US-08-986-304-2	Sequence 2, Appl1
C 425	13	2.3	730	2	US-08-734-591A-147	Sequence 147, App	C 497	13	2.3	1133	1	US-07-750-080A-2	Sequence 2, Appl1
C 426	13	2.3	730	2	US-08-469-660-147	Sequence 147, App	C 498	13	2.3	1133	4	US-07-750-080A-3	Sequence 3, Appl1
C 427	13	2.3	730	4	US-08-341-018-47	Sequence 47, Appl1	C 499	13	2.3	1133	4	US-08-651-472-2	Sequence 2, Appl1
C 428	13	2.3	730	4	US-08-470-335-147	Sequence 147, App	C 500	13	2.3	1151	1	US-08-651-472-3	Sequence 3, Appl1
C 429	13	2.3	730	4	US-08-735-021-147	Sequence 147, App	C 501	13	2.3	1151	1	US-08-236-754-3	Sequence 3, Appl1
C 430	13	2.3	730	4	US-08-734-664A-147	Sequence 147, App	C 502	13	2.3	1158	1	US-08-891-254-4	Sequence 4, Appl1
C 431	13	2.3	730	5	PCT-US94-05083C-143	Sequence 143, App	C 503	13	2.3	1158	2	US-08-819-539-4	Sequence 4, Appl1
C 432	13	2.3	730	5	PCT-US95-06846A-147	Sequence 147, App	C 504	13	2.3	1158	5	PCT-US93-06243-4	Sequence 4, Appl1
C 433	13	2.3	804	1	US-08-411-635-1	Sequence 1, Appl1	C 505	13	2.3	1158	5	PCT-US96-08819-4	Sequence 4, Appl1
C 434	13	2.3	804	5	PCT-US94-10644-1	Sequence 1, Appl1	C 506	13	2.3	1161	3	US-08-689-421-22	Sequence 22, Appl1
C 435	13	2.3	807	2	US-08-531-927B-9	Sequence 9, Appl1	C 507	13	2.3	1161	4	US-09-389-528-22	Sequence 22, Appl1
436	13	2.3	816	2	US-08-822-028-26	Sequence 26, Appl1	C 508	13	2.3	1169	4	US-08-307-591-2	Sequence 2, Appl1
437	13	2.3	816	4	US-08-479-285-25	Sequence 25, Appl1	C 509	13	2.3	1199	4	US-09-080-965-1	Sequence 1, Appl1
438	13	2.3	819	2	US-08-822-028-25	Sequence 25, Appl1	C 510	13	2.3	1200	1	US-08-040-548-32	Sequence 32, Appl1
439	13	2.3	819	4	US-08-479-285-25	Sequence 25, Appl1	C 511	13	2.3	1200	1	US-08-466-344-32	Sequence 32, Appl1
440	13	2.3	834	2	US-08-569-168-3	Sequence 3, Appl1	C 512	13	2.3	1200	6	5206152-8	Patent No. 5206152
441	13	2.3	837	2	US-08-569-168-1	Sequence 1, Appl1	C 513	13	2.3	1209	1	US-07-750-080A-22	Sequence 22, Appl1
442	13	2.3	839	1	US-08-474-633A-93	Sequence 93, Appl1	C 514	13	2.3	1209	2	US-08-200-724A-4	Sequence 4, Appl1
443	13	2.3	839	4	US-09-276-531-110	Sequence 110, App	C 515	13	2.3	1209	4	US-08-651-472-22	Sequence 22, Appl1
444	13	2.3	839	5	PCT-US93-02480-16	Sequence 16, Appl1	C 516	13	2.3	1209	4	US-08-851-376A-4	Sequence 4, Appl1
C 445	13	2.3	842	2	US-08-820-170A-3	Sequence 3, Appl1	C 517	13	2.3	1221	4	US-08-445-090-1	Sequence 1, Appl1
C 446	13	2.3	842	3	US-09-055-669-3	Sequence 3, Appl1	C 518	13	2.3	1221	4	US-09-286-691-13	Sequence 13, Appl1
C 447	13	2.3	842	4	US-09-273-565-3	Sequence 3, Appl1	C 519	13	2.3	1242	4	US-09-147-928-1	Sequence 1, Appl1
448	13	2.3	847	4	US-09-260-283-1	Sequence 1, Appl1	C 520	13	2.3	1242	6	5240845-2	Patent No. 5240845
449	13	2.3	859	4	US-09-247-373B-47	Sequence 47, Appl1	C 521	13	2.3	1250	1	US-08-117-083-59	Sequence 59, Appl1
450	13	2.3	860	4	US-08-975-762-31	Sequence 31, Appl1	C 522	13	2.3	1257	1	US-07-946-232-7	Sequence 7, Appl1
451	13	2.3	862	2	US-08-822-028-5	Sequence 5, Appl1	C 523	13	2.3	1260	3	US-08-793-331-1	Sequence 1, Appl1
452	13	2.3	862	4	US-08-479-285-5	Sequence 5, Appl1	C 524	13	2.3	1262	6	5240845-3	Patent No. 5240845
453	13	2.3	865	2	US-08-822-028-3	Sequence 3, Appl1	C 525	13	2.3	1265	6	5198542-5	Patent No. 5198542
454	13	2.3	865	4	US-08-479-285-3	Sequence 3, Appl1	C 526	13	2.3	1272	1	US-08-073-799C-7	Sequence 7, Appl1
455	13	2.3	879	4	US-09-029-213B-1	Sequence 1, Appl1	C 527	13	2.3	1272	1	US-07-947-672-7	Sequence 7, Appl1
C 456	13	2.3	912	3	US-08-688-988-3	Sequence 3, Appl1	C 528	13	2.3	1272	1	US-08-433-043-7	Sequence 7, Appl1
C 457	13	2.3	917	1	US-07-949-812-1	Sequence 1, Appl1	C 529	13	2.3	1272	2	US-08-660-963-7	Sequence 7, Appl1
458	13	2.3	924	1	US-07-593-657-4	Sequence 4, Appl1	C 530	13	2.3	1272	2	US-08-569-168-6	Sequence 6, Appl1
C 459	13	2.3	957	1	US-08-684-862-11	Sequence 11, Appl1	C 531	13	2.3	1275	3	US-08-725-532A-2	Sequence 2, Appl1
460	13	2.3	966	2	US-08-286-815A-1	Sequence 1, Appl1	C 532	13	2.3	1284	3	US-08-331-625A-2	Sequence 42, Appl1
461	13	2.3	966	3	US-08-980-357-1	Sequence 1, Appl1	C 533	13	2.3	1287	5	PCT-US93-06243-3	Sequence 3, Appl1
462	13	2.3	967	1	US-08-460-860-1	Sequence 1, Appl1	C 534	13	2.3	1288	2	US-08-200-724A-4	Sequence 4, Appl1
463	13	2.3	968	5	PCT-US94-04208-1	Sequence 1, Appl1	C 535	13	2.3	1288	2	US-09-030-270A-3	Sequence 3, Appl1
464	13	2.3	977	5	PCT-US94-04208-11	Sequence 11, Appl1	C 536	13	2.3	1288	4	US-08-851-376A-3	Sequence 3, Appl1
465	13	2.3	982	2	US-08-822-028-1	Sequence 1, Appl1	C 537	13	2.3	1306	2	US-08-671-975A-1	Sequence 1, Appl1
							C 538	13	2.3	1310	1	US-08-311-023-1	Sequence 1, Appl1

539	13	2.3	1320	1	US-08-257-073-15	Sequence 15, Appl	C 612	13	2.3	1764	4	US-08-734-664A-150	Sequence 150, App
540	13	2.3	1343	2	US-08-307-588-1	Sequence 1, Appl	C 613	13	2.3	1764	5	PCT-US94-05083C-146	Sequence 146, App
541	13	2.3	1368	4	US-08-972-927-8	Sequence 8, Appl	C 614	13	2.3	1764	5	PCT-US95-06846A-150	Sequence 150, App
C 542	13	2.3	1404	1	US-07-985-458-2	Sequence 2, Appl	C 615	13	2.3	1776	2	US-08-531-927B-1	Sequence 1, Appl
543	13	2.3	1422	1	US-08-439-725A-1	Sequence 1, Appl	C 616	13	2.3	1776	3	US-08-655-352-10	Sequence 10, Appl
544	13	2.3	1422	2	US-08-867-471-1	Sequence 1, Appl	C 617	13	2.3	1796	3	PCT-US95-10904-65	Sequence 65, Appl
545	13	2.3	1422	3	US-08-705-245-18	Sequence 18, Appl	C 618	13	2.3	1820	2	US-08-389-561B-17	Sequence 17, Appl
546	13	2.3	1422	5	PCT-US96-06664-1	Sequence 1, Appl	C 619	13	2.3	1820	3	US-08-466-047B-17	Sequence 17, Appl
547	13	2.3	1423	2	US-08-948-616-4	Sequence 4, Appl	C 620	13	2.3	1831	1	US-08-101-435-3	Sequence 3, Appl
548	13	2.3	1423	2	US-09-193-510-4	Sequence 4, Appl	C 621	13	2.3	1831	2	US-08-455-073A-3	Sequence 3, Appl
549	13	2.3	1423	4	US-09-368-402-4	Sequence 4, Appl	C 622	13	2.3	1882	1	US-08-696-349-1	Sequence 1, Appl
C 550	13	2.3	1432	5	PCT-US94-12912-4	Sequence 4, Appl	C 623	13	2.3	1882	2	PCT-US96-13156-1	Sequence 1, Appl
C 551	13	2.3	1450	4	US-09-108-020-15	Sequence 15, Appl	C 624	13	2.3	1892	2	US-08-933-750C-66	Sequence 66, Appl
C 552	13	2.3	1453	2	US-08-169-948B-9	Sequence 9, Appl	C 625	13	2.3	1892	4	US-09-234-613-66	Sequence 66, Appl
C 553	13	2.3	1453	2	US-08-448-873-9	Sequence 9, Appl	C 626	13	2.3	1898	1	US-08-063-552-12	Sequence 12, Appl
C 554	13	2.3	1455	4	US-09-276-531-33	Sequence 33, Appl	C 627	13	2.3	1898	5	PCT-US93-05704-12	Sequence 12, Appl
C 555	13	2.3	1476	4	US-08-896-346-1	Sequence 1, Appl	C 628	13	2.3	1926	1	US-07-718-535-5	Sequence 5, Appl
C 556	13	2.3	1479	3	US-09-008-636-2	Sequence 2, Appl	C 629	13	2.3	1926	1	US-08-161-999-5	Sequence 5, Appl
C 557	13	2.3	1479	3	US-09-006-636-3	Sequence 3, Appl	C 630	13	2.3	1935	6	5198542-3	Patent No. 5198542
C 558	13	2.3	1479	4	US-09-006-632-2	Sequence 2, Appl	C 631	13	2.3	1955	1	US-08-487-890A-114	Sequence 114, App
C 559	13	2.3	1479	4	US-09-006-632-3	Sequence 3, Appl	C 632	13	2.3	1955	2	US-08-478-435-114	Sequence 114, App
C 560	13	2.3	1507	1	US-07-641-143B-1	Sequence 1, Appl	C 633	13	2.3	1955	2	US-08-337-483-114	Sequence 114, App
C 561	13	2.3	1507	1	US-07-641-143B-1	Sequence 1, Appl	C 634	13	2.3	1955	2	US-08-478-373-114	Sequence 114, App
C 562	13	2.3	1507	1	US-08-124-290-1	Sequence 1, Appl	C 635	13	2.3	1955	3	US-08-474-671-114	Sequence 114, App
C 563	13	2.3	1507	1	US-08-124-290-1	Sequence 1, Appl	C 636	13	2.3	1955	3	US-08-483-577A-114	Sequence 114, App
C 564	13	2.3	1507	3	US-08-696-372A-1	Sequence 1, Appl	C 637	13	2.3	1974	1	US-08-413-135-3	Sequence 3, Appl
C 565	13	2.3	1507	3	US-08-696-372A-1	Sequence 1, Appl	C 638	13	2.3	1974	1	US-08-413-135-3	Sequence 3, Appl
C 566	13	2.3	1549	2	US-08-865-597A-1	Sequence 1, Appl	C 639	13	2.3	1975	3	US-09-413-452-4	Sequence 4, Appl
C 567	13	2.3	1561	1	US-07-968-971A-3	Sequence 3, Appl	C 640	13	2.3	1985	4	US-08-619-812-1	Sequence 1, Appl
C 568	13	2.3	1561	1	US-07-824-247-44	Sequence 44, Appl	C 641	13	2.3	2000	2	US-09-036-582-35	Sequence 35, Appl
C 569	13	2.3	1561	1	US-08-142-473A-4	Sequence 4, Appl	C 642	13	2.3	2035	3	US-08-705-937-7	Sequence 7, Appl
C 570	13	2.3	1561	1	US-08-469-203A-4	Sequence 4, Appl	C 643	13	2.3	2035	3	US-09-022-699-3	Sequence 3, Appl
C 571	13	2.3	1561	1	US-08-469-203A-4	Sequence 4, Appl	C 644	13	2.3	2035	5	PCT-US93-12464-1	Sequence 1, Appl
C 572	13	2.3	1561	3	US-08-470-204A-4	Sequence 44, Appl	C 645	13	2.3	2037	1	US-08-844-086-1	Sequence 1, Appl
C 573	13	2.3	1577	3	US-08-691-563C-89	Sequence 89, Appl	C 646	13	2.3	2044	2	US-08-071-601-3	Sequence 3, Appl
C 574	13	2.3	1578	1	US-08-188-582-29	Sequence 29, Appl	C 647	13	2.3	2044	2	US-08-621-100-3	Sequence 3, Appl
C 575	13	2.3	1578	1	US-08-646-715-29	Sequence 29, Appl	C 648	13	2.3	2060	1	US-07-721-761A-31	Sequence 31, Appl
576	13	2.3	1601	3	US-08-817-188-3	Sequence 3, Appl	C 649	13	2.3	2060	4	US-07-978-687-31	Sequence 31, Appl
577	13	2.3	1636	6	5447867-2	Patent No. 5447867	C 650	13	2.3	2060	4	US-09-705-143-1	Sequence 1, Appl
C 578	13	2.3	1650	2	US-08-770-54A-5	Sequence 5, Appl	C 651	13	2.3	2060	5	PCT-US91-01750-2	Sequence 2, Appl
C 579	13	2.3	1659	2	US-08-916-902A-2	Sequence 2, Appl	C 652	13	2.3	2060	5	PCT-US91-05801-31	Sequence 31, Appl
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C 582	13	2.3	1678	1	US-08-384-556A-6	Sequence 6, Appl	C 655	13	2.3	2075	3	US-08-750-391-7	Sequence 7, Appl
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C 584	13	2.3	1678	5	PCT-US94-12364-10	Sequence 10, Appl	C 657	13	2.3	2081	5	PCT-US91-01750-3	Sequence 3, Appl
C 585	13	2.3	1678	5	PCT-US95-07753-6	Sequence 6, Appl	C 658	13	2.3	2085	2	US-08-283-917-8	Sequence 8, Appl
C 586	13	2.3	1680	2	US-08-700-152A-3	Sequence 3, Appl	C 659	13	2.3	2085	2	US-08-661-716-8	Sequence 8, Appl
587	13	2.3	1690	2	US-08-461-812-3	Sequence 3, Appl	C 660	13	2.3	2097	2	US-08-655-345-3	Sequence 3, Appl
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598	13	2.3	1760	4	US-09-374-824-8	Sequence 8, Appl	C 671	13	2.3	2191	1	US-08-81-891-72	Sequence 72, Appl
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C 690	13	2.3	2268	4	US-09-050-159-133	Sequence 133, App	C 763	13	2.3	2734	6	5304637-26	Patent No. 5304637
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C 697	13	2.3	2310	4	US-08-956-182-13	Sequence 13, Appl1	C 770	13	2.3	2784	2	US-08-466-974-1	Sequence 1, Appl1
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-602-359A-2

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Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 31 AATCATACACTAAGCATAG 11

RESULT 3
US-08-602-359A-1
Sequence 1, Application US/08602359A
Patent No. 5942430
GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
APPLICANT: MURPHY, Dennis
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APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald V.
APPLICANT: WARREN, Patrick V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-602-359A-1

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Best Local Similarity 100.0%; Pred. No. 0.095;
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RESULT 4
US-08-781-891-207/C
Sequence 207, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Yang-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
TITLE OF INVENTION: WERNER'S SYNDROME
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052,419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-207

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Best Local Similarity 100.0%; Pred. No. 3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 99 ATGCTTAATATATGCAA 116
|||||
DB 29176 ATGCTTAATATATGCAA 29159

RESULT 5
5256558-7/c
PATENT NO. 5256558
APPLICANT: CORUZZI, GLORIA M.; TSAI, FONG-YING
TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/514, 816
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,302
FILING DATE: 03-MAY-1989
SEQ ID NO: 7
LENGTH: 1121
5256558-7

Query Match 3.1%; Score 17; DB 6; Length 1121;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 336 AGTATGTTTCTTAT.352
|||||
DB 798 AGTATGTTTCTTAT 782

RESULT 6
US-08-549-515-4
Sequence 4, Application US/08549515
Patent No. 6054123
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Klein, Michael H
TITLE OF INVENTION: Haemophilus Influenzae
TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 Unversity Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549, 515
FILING DATE: 27-OCT-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-522
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-549-515-4

Query Match 2.9%; Score 16; DB 3; Length 837;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 112 TGGAAATATGATTTAA 127
|||||
DB 430 TGGAAATATGATTTAA 445

RESULT 7
US-08-897-340-4/c
Sequence 4, Application US/08897340
Patent No. 5955306
GENERAL INFORMATION:
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
TITLE OF INVENTION: Weight Control Pathway Genes and Uses
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,340
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/715,032
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silverl, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-005CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-897-340-4

Query Match 2.9%; Score 16; DB 2; Length 1700;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 335 CAGTATGTTTCTT 350
|||||
DB 1604 CAGTATGTTTCTT 1589

RESULT 8
US-09-252-329-4/c
Sequence 4, Application US/09252329
Patent No. 6147192
GENERAL INFORMATION:
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
TITLE OF INVENTION: Weight Control Pathway Genes and Uses
Therefor

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,329
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/897,340
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNT-005CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-252-329-4

Query Match 2.9%; Score 16; DB 4; Length 1700;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 CAGTATTTCTTCTTCT 350
DB 1604 CAGTATTTCTTCTTCT 1589

RESULT 9
US-08-464-340A-3/C
Sequence 3, Application US/08464340A
Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08464,340A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: cDNA
US-08-464-340A-3

Query Match 2.9%; Score 16; DB 1; Length 2483;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTATCTGATGTCGTC 98
DB 760 CTATCTGATGTCGTC 745

RESULT 10
PCT-US94-08449A-3/C
Sequence 3, Application PC/TUS9408449A
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Potassium Channel Protein 1 and 2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
FILING DATE: SUBMITTED HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: cDNA
PCT-US94-08449A-3

Query Match 2.9%; Score 16; DB 5; Length 2483;
Best Local Similarity 100.0%; Pred. No. 32;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 CTATCTCTATGTCGTC 98
|||||

Db 760 CTATCTCTATGTCGTC 745

RESULT 11
US-08-703-809-2/c
Sequence 2, Application US/08703809
Patent No. 5716808
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: GENETIC ENGINEERING OF PICHIA METHANOLICA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,809
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 96-18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-703-809-2

Query Match 2.9%; Score 16; DB 1; Length 3386;
Best Local Similarity 100.0%; Pred. NO. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 GTTATAGTTGCTTTAA 220
|||||

Db 1225 GTTATAGTTGCTTTAA 1210

RESULT 12
US-08-703-808-2/c
Sequence 2, Application US/08703808
Patent No. 5736383
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: PREPARATION OF PICHIA METHANOLICA AUXOTROPHIC
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,808
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 96-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-703-808-2

Query Match 2.9%; Score 16; DB 1; Length 3386;
Best Local Similarity 100.0%; Pred. NO. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 GTTATAGTTGCTTTAA 220
|||||

Db 1225 GTTATAGTTGCTTTAA 1210

RESULT 13
US-08-914-066-2/c
Sequence 2, Application US/08914066
Patent No. 5854039
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: TRANSFORMATION OF PICHIA METHANOLICA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,066
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E.
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-37

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-914-066-2

Query Match 2.9%; Score 16; DB 2; Length 3386;
Best local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 205 GTTATAGTTGGTTAA 220
|||||
Db 1225 GTTATAGTTGGTTAA 1210

RESULT 14
US-08-703-807-2/C
Sequence 2, Application US/08703807
Patent No. 5955349
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDES IN PICHIA METANOLICA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,807
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 96-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-703-807-2

Query Match 2.9%; Score 16; DB 2; Length 3386;

Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 205 GTTATAGTTGGTTAA 220
|||||
Db 1225 GTTATAGTTGGTTAA 1210

RESULT 15
US-08-747-108A-2/C
Sequence 2, Application US/08747108A
Patent No. 5965389
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: PRODUCTION OF GAD65 IN METHYLOTROPHIC YEAST
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 98111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,108A
FILING DATE: 96-NOV-08
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-23-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-747-108A-2

Query Match 2.9%; Score 16; DB 2; Length 3386;
Best local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 205 GTTATAGTTGGTTAA 220
|||||
Db 1225 GTTATAGTTGGTTAA 1210

Search completed: May 31, 2001, 02:15:13
Job time: 4444 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2001, 23:54:33 ; Search time 1105.94 Seconds
(without alignments)
4384.085 Million cell updates/sec

Title: us-09-382-242-23

Perfect score: 555
Sequence: 1 ATGCTTTAAACAAGCACTC.....AATCATACACTAAACGATAG 555

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9623517 seqs, 4368049070 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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 212: gb_gss12:*
 213: gb_gss13:*
 214: gb_gss14:*
 215: gb_gss15:*
 216: gb_gss16:*
 217: gb_gss17:*
 218: gb_gss18:*
 219: gb_gss19:*
 220: gb_gss20:*
 221: gb_gss21:*
 222: gb_gss22:*
 223: gb_gss23:*
 224: gb_gss24:*
 225: gb_gss25:*
 226: gb_gss26:*
 227: gb_gss27:*
 228: gb_gss28:*
 229: gb_gss29:*
 230: gb_gss30:*
 231: gb_gss31:*
 232: gb_gss32:*
 233: gb_gss33:*
 234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	3.8	671	143	Bf071768	Bf071768 db57a08.x
2	21	3.8	745	203	AQ210775	AQ210775 HS_2229.A
3	20	3.6	225	162	BE072277	BE072277 QV4-BF053
4	20	3.6	404	170	BP906208	BP906208 IL3-MT026
5	20	3.6	667	223	A2502214	A2502214 1M0341301
6	20	3.6	668	212	A0854708	A0854708 CPG2172A
7	20	3.6	771	230	CNS01VPE	AL169403 Tetraodon
8	20	3.6	983	230	CNS03B2I	AL237159 Tetraodon
9	20	3.6	1016	231	CNS0421Y	AL270943 Tetraodon
10	20	3.6	1019	231	CNS03009	AL253602 Tetraodon
11	19	3.4	223	29	AV374815	AV374815 AV374815
12	19	3.4	263	174	BG148611	BG148611 uu84g06.y
13	19	3.4	288	159	X61840	X61840 MOSTSG129X
14	19	3.4	291	129	BB266564	BB266564 BB266564
15	19	3.4	302	148	BF460484	BF460484 UI-M-CG0P
16	19	3.4	326	19	AI363223	AI363223 qy56b01.x
17	19	3.4	375	3	AA175663	AA175663 ms37f07.r
18	19	3.4	388	208	AO567554	AO567554 HS_2118_B

19	19	3.4	410	AA451408	vfc1c07.r	92	18	3.2	355	117	AM569772	hg20h01.x	19	19	3.2	355	117	AM569772	hg20h01.x
20	19	3.4	416	B6095176	u8b4906.x	93	18	3.2	355	148	BF475300	7c07f11.x	20	19	3.2	355	148	BF475300	7c07f11.x
21	19	3.4	434	BE473522	sp52404.y	94	18	3.2	355	218	AZ245251	RPCI-23-3	21	19	3.2	355	218	AZ245251	RPCI-23-3
22	19	3.4	462	AA260892	va01h12.r	95	18	3.2	355	127	B43580	HS-1058-A1-	22	19	3.2	355	127	B43580	HS-1058-A1-
23	19	3.4	486	A1875162	u130c07.x	96	18	3.2	356	167	BE502815	hz79g02.x	23	19	3.2	356	167	BE502815	hz79g02.x
24	19	3.4	497	BF228048	uz39a12.x	97	18	3.2	356	213	AQ919017	RPCI-23-2	24	19	3.2	356	213	AQ919017	RPCI-23-2
25	19	3.4	502	AQ236170	HS_-2058.B	98	18	3.2	357	220	AZ387436	IM016L15	25	19	3.2	357	220	AZ387436	IM016L15
26	19	3.4	510	AQ180776	HS_3220.A	99	18	3.2	358	18	A1290798	qm13b09.x	26	19	3.2	358	18	A1290798	qm13b09.x
27	19	3.4	533	AZ365242	IM0111N14	100	18	3.2	359	164	BE220020	hw66a10.x	27	19	3.2	359	164	BE220020	hw66a10.x
28	19	3.4	534	AQ439999	HS_5073.A	101	18	3.2	361	102	A18060106	v406802.x	28	19	3.2	361	102	A18060106	v406802.x
29	19	3.4	557	AA212780	mw84e07.r	102	18	3.2	363	167	BE465398	hw15g08.x	29	19	3.2	363	167	BE465398	hw15g08.x
30	19	3.4	572	AZ601840	IM0420L16	103	18	3.2	364	216	AZ093444	RPCI-24-8	30	19	3.2	364	216	AZ093444	RPCI-24-8
31	19	3.4	588	BE111788	UT-R-BU1-	104	18	3.2	364	226	AZ737138	RPCI-23-1	31	19	3.2	364	226	AZ737138	RPCI-23-1
32	19	3.4	620	AQ779389	HS_3207_B	105	18	3.2	368	218	AZ238857	RPCI-23-8	32	19	3.2	368	218	AZ238857	RPCI-23-8
33	19	3.4	629	AZ624727	IM0463A15	106	18	3.2	379	215	AZ030575	RPCI-23-3	33	19	3.2	379	215	AZ030575	RPCI-23-3
34	19	3.4	677	AZ627350	IM0469A11	107	18	3.2	383	12	AA807377	tx05b05.s	34	19	3.2	383	12	AA807377	tx05b05.s
35	19	3.4	733	BE533804	601233070	108	18	3.2	384	214	AZ012435	RPCI-23-3	35	19	3.2	384	214	AZ012435	RPCI-23-3
36	19	3.4	740	AQ194413	RPCI11_-45	109	18	3.2	389	32	AA020928	dl16e03.y	36	19	3.2	389	32	AA020928	dl16e03.y
37	19	3.4	794	B02432	GSRU_-153e12	110	18	3.2	393	226	AZ748353	RPCI-24-6	37	19	3.2	393	226	AZ748353	RPCI-24-6
38	19	3.2	113	AZ224689	RPCI-23-6	111	18	3.2	399	103	A1913486	t289a12.x	38	19	3.2	399	103	A1913486	t289a12.x
39	19	3.2	118	AZ259802	RPCI-23-1	112	18	3.2	401	215	AZ029663	ys15h12.r1	39	19	3.2	401	215	AZ029663	ys15h12.r1
40	19	3.2	132	AM325382	16330.MAR	113	18	3.2	403	153	H71945	ys15h12.r1	40	19	3.2	403	153	H71945	ys15h12.r1
41	19	3.2	133	AZ482850	IM0308P07	114	18	3.2	403	226	AZ715894	RPCI-24-8	41	19	3.2	403	226	AZ715894	RPCI-24-8
42	19	3.2	137	AZ083432	RPCI-23-5	115	18	3.2	404	220	AZ372443	RPCI-23-7	42	19	3.2	404	220	AZ372443	RPCI-23-7
43	19	3.2	145	AZ240661	RPCI-23-7	116	18	3.2	405	223	AZ562251	RPCI-23-2	43	19	3.2	405	223	AZ562251	RPCI-23-2
44	19	3.2	147	AZ113521	RPCI-23-4	117	18	3.2	408	214	AQ986297	RPCI-23-2	44	19	3.2	408	214	AQ986297	RPCI-23-2
45	19	3.2	160	AZ720211	RPCI-24-1	118	18	3.2	411	223	AZ563016	RPCI-23-2	45	19	3.2	411	223	AZ563016	RPCI-23-2
46	19	3.2	167	AZ116215	RPCI-23-4	119	18	3.2	415	218	AZ266835	RPCI-23-1	46	19	3.2	415	218	AZ266835	RPCI-23-1
47	18	3.2	188	AZ116181	RPCI-23-4	120	18	3.2	417	218	AZ243617	RPCI-23-7	47	18	3.2	417	218	AZ243617	RPCI-23-7
48	18	3.2	190	AZ7199882	RPCI-24-8	121	18	3.2	417	220	AZ345840	IM0080P10	48	18	3.2	417	220	AZ345840	IM0080P10
49	18	3.2	191	AZ009468	RPCI-23-3	122	18	3.2	418	216	AZ132390	OSJNB006	49	18	3.2	418	216	AZ132390	OSJNB006
50	18	3.2	198	AZ713308	RPCI-24-1	123	18	3.2	418	218	AZ265130	RPCI-23-4	50	18	3.2	418	218	AZ265130	RPCI-23-4
51	18	3.2	204	AZ742009	RPCI-24-9	124	18	3.2	419	161	BE022026	sm65f02.y	51	18	3.2	419	161	BE022026	sm65f02.y
52	18	3.2	210	AZ005900	RPCI-23-3	125	18	3.2	421	106	AU015094	AU015094	52	18	3.2	421	106	AU015094	AU015094
53	18	3.2	216	AZ695472	RPCI-23-2	126	18	3.2	421	226	AZ749592	RPCI-24-1	53	18	3.2	421	226	AZ749592	RPCI-24-1
54	18	3.2	223	AZ704685	RPCI-23-2	127	18	3.2	423	218	AZ245869	RPCI-23-7	54	18	3.2	423	218	AZ245869	RPCI-23-7
55	18	3.2	228	AZ282258	RPCI-23-1	128	18	3.2	424	226	AZ737924	RPCI-24-1	55	18	3.2	424	226	AZ737924	RPCI-24-1
56	18	3.2	230	AZ211190	IM0184H07	129	18	3.2	426	221	AZ401163	RPCI-23-4	56	18	3.2	426	221	AZ401163	RPCI-23-4
57	18	3.2	236	AZ259028	RPCI-23-1	130	18	3.2	430	223	AZ555575	RPCI-23-2	57	18	3.2	430	223	AZ555575	RPCI-23-2
58	18	3.2	239	AZ742810	RPCI-24-1	131	18	3.2	430	229	CNS0009S	AL086280	58	18	3.2	430	229	CNS0009S	AL086280
59	18	3.2	251	AZ747559	RPCI-24-9	132	18	3.2	431	214	AQ987979	RPCI-23-3	59	18	3.2	431	214	AQ987979	RPCI-23-3
60	18	3.2	253	AZ276686	RPCI-23-1	133	18	3.2	431	214	AZ006374	RPCI-23-3	60	18	3.2	431	214	AZ006374	RPCI-23-3
61	18	3.2	256	AQ983564	RPCI-23-3	134	18	3.2	431	218	AZ251064	RPCI-23-4	61	18	3.2	431	218	AZ251064	RPCI-23-4
62	18	3.2	256	AZ719156	RPCI-24-7	135	18	3.2	432	216	AZ114730	RPCI-23-4	62	18	3.2	432	216	AZ114730	RPCI-23-4
63	18	3.2	261	AV329696	AV329696	136	18	3.2	434	204	AQ055399	CIT-HSP-2	63	18	3.2	434	204	AQ055399	CIT-HSP-2
64	18	3.2	262	AZ013629	RPCI-23-2	137	18	3.2	435	241	AQ982226	RPCI-23-3	64	18	3.2	435	241	AQ982226	RPCI-23-3
65	18	3.2	265	AZ064469	RPCI-23-4	138	18	3.2	436	214	AZ009332	RPCI-23-3	65	18	3.2	436	214	AZ009332	RPCI-23-3
66	18	3.2	266	AZ282824	RPCI-23-1	139	18	3.2	436	216	AZ099089	RPCI-23-4	66	18	3.2	436	216	AZ099089	RPCI-23-4
67	18	3.2	272	AZ231992	RPCI-23-8	140	18	3.2	437	214	AQ976760	RPCI-23-8	67	18	3.2	437	214	AQ976760	RPCI-23-8
68	18	3.2	275	A1825156	wa93b08.x	141	18	3.2	438	214	AZ011981	RPCI-23-2	68	18	3.2	438	214	AZ011981	RPCI-23-2
69	18	3.2	277	AQ928602	RPCI-23-2	142	18	3.2	438	218	AZ247682	RPCI-23-9	69	18	3.2	438	218	AZ247682	RPCI-23-9
70	18	3.2	279	CNS000E5	AL083099	143	18	3.2	438	221	AZ395428	RPCI-23-9	70	18	3.2	438	221	AZ395428	RPCI-23-9
71	18	3.2	287	AZ420051	IM0196M14	144	18	3.2	438	224	AZ631727	RPCI-23-8	71	18	3.2	438	224	AZ631727	RPCI-23-8
72	18	3.2	289	AZ001421	RPCI-23-3	145	18	3.2	443	218	AZ233637	RPCI-23-8	72	18	3.2	443	218	AZ233637	RPCI-23-8
73	18	3.2	294	AZ718988	RPCI-24-1	146	18	3.2	444	205	AQ335676	HS_5015.B	73	18	3.2	444	205	AQ335676	HS_5015.B
74	18	3.2	295	AZ076745	RPCI-23-4	147	18	3.2	446	221	AZ444543	IM0239I18	74	18	3.2	446	221	AZ444543	IM0239I18
75	18	3.2	298	AZ027796	RPCI-23-3	148	18	3.2	449	225	AZ641899	RPCI-23-2	75	18	3.2	449	225	AZ641899	RPCI-23-2
76	18	3.2	300	AZ718475	RPCI-24-1	149	18	3.2	450	213	AQ928778	RPCI-23-2	76	18	3.2	450	213	AQ928778	RPCI-23-2
77	18	3.2	310	BB258093	BB258093	150	18	3.2	450	213	AZ016668	RPCI-23-2	77	18	3.2	450	213	AZ016668	RPCI-23-2
78	18	3.2	312	AZ267463	RPCI-23-1	151	18	3.2	450	226	AZ753606	RPCI-24-1	78	18	3.2	450	226	AZ753606	RPCI-24-1
79	18	3.2	314	AZ273456	RPCI-23-8	152	18	3.2	451	219	AZ295119	RPCI-23-1	79	18	3.2	451	219	AZ295119	RPCI-23-1
80	18	3.2	315	AZ096156	RPCI-23-4	153	18	3.2	452	213	AQ916497	nbep00650	80	18	3.2	452	213	AQ916497	nbep00650
81	18	3.2	316	AQ548184	RPCI-11-4	154	18	3.2	452	213	AQ931484	RPCI-23-2	81	18	3.2	452	213	AQ931484	RPCI-23-2
82	18	3.2	320	AZ722583	RPCI-24-9	155	18	3.2	454	120	AA818937	RC0-ST028	82	18	3.2	454	120	AA818937	RC0-ST028
83	18	3.2	322	BB536188	BB536188	156	18	3.2	454	215	AZ074421	RPCI-23-3	83	18	3.2	454	215	AZ074421	RPCI-23-3
84	18	3.2	326	AZ721677	RPCI-24-7	157	18	3.2	454	220	AZ349718	IM0086013	84	18	3.2	454	220	AZ349718	IM0086013
85	18	3.2	327	AZ610200	IM0435C24	158	18	3.2	457	213	AQ931339	RPCI-23-2	85	18	3.2	457	213	AQ931339	RPCI-23-2
86	18	3.2	336	BB549290	BB549290	159	18	3.2	460	119	AA757259	s133a02.y	86						

165	18	3.2	466	226	AZ712633	AZ712633	RPCI-24-1	C 238	18	3.2	551	216	AZ095093	AZ095093	RPCI-23-4
C 166	18	3.2	467	20	A1434898	A1434898	RPCI-23-3	C 239	18	3.2	552	214	AQ978397	AQ978397	RPCI-23-3
C 167	18	3.2	467	20	AZ004487	AZ004487	RPCI-23-3	C 240	18	3.2	552	223	AZ510422	AZ510422	RPCI-23-3
C 168	18	3.2	468	224	AZ611193	AZ611193	IM0436A05	C 241	18	3.2	553	138	BE672435	BE672435	x
C 169	18	3.2	471	137	BE655506	BE655506	UI-M-BHO-	C 242	18	3.2	553	219	AZ292238	AZ292238	RPCI-23-1
C 170	18	3.2	471	226	AZ739240	AZ739240	RPCI-24-1	C 243	18	3.2	554	219	AZ291506	AZ291506	RPCI-23-1
C 171	18	3.2	472	213	AQ913820	AQ913820	nbe00045K	C 244	18	3.2	554	222	AZ461909	AZ461909	RPCI-23-1
C 172	18	3.2	474	167	BE501062	BE501062	7a36d09.x	C 245	18	3.2	555	214	AQ979246	AQ979246	RPCI-23-2
C 173	18	3.2	475	216	AZ093932	AZ093932	RPCI-23-4	C 246	18	3.2	556	223	AZ559347	AZ559347	RPCI-23-2
C 174	18	3.2	475	220	AZ38756	AZ38756	IM0148L20	C 247	18	3.2	558	228	AZ559347	AZ559347	RPCI-23-1
C 175	18	3.2	476	225	AZ639424	AZ639424	IM0499J22	C 248	18	3.2	561	168	BF716302	BF716302	RPCI-23-1
C 176	18	3.2	477	216	AZ085526	AZ085526	RPCI-23-3	C 249	18	3.2	563	215	AZ021734	AZ021734	RPCI-23-3
C 177	18	3.2	478	210	AQ095415	AQ095415	HS-2148.A	C 250	18	3.2	565	215	AZ080645	AZ080645	RPCI-23-3
C 178	18	3.2	479	223	AZ555234	AZ555234	RPCI-23-1	C 251	18	3.2	565	221	AZ410398	AZ410398	IM0182008
C 179	18	3.2	479	226	AZ742723	AZ742723	RPCI-24-1	C 252	18	3.2	570	8	AA516727	AA516727	vh84a11.r
C 180	18	3.2	480	211	AO808330	AO808330	HS-5261.B	C 253	18	3.2	570	209	AO670144	AO670144	HS-5332.B
C 181	18	3.2	480	218	AZ237827	AZ237827	RPCI-23-7	C 254	18	3.2	571	218	AZ285046	AZ285046	RPCI-23-1
C 182	18	3.2	481	214	AZ008924	AZ008924	RPCI-23-3	C 255	18	3.2	572	214	AZ000786	AZ000786	RPCI-23-3
C 183	18	3.2	482	219	AZ294530	AZ294530	RPCI-23-1	C 256	18	3.2	572	224	AZ624233	AZ624233	IM0462G15
C 184	18	3.2	483	218	AZ231912	AZ231912	RPCI-23-9	C 257	18	3.2	572	226	AZ738666	AZ738666	RPCI-24-1
C 185	18	3.2	484	215	AZ051461	AZ051461	RPCI-23-3	C 258	18	3.2	574	215	AZ039495	AZ039495	RPCI-23-3
C 186	18	3.2	484	220	AZ383877	AZ383877	IM0141M07	C 259	18	3.2	574	226	AZ728890	AZ728890	RPCI-24-1
C 187	18	3.2	486	214	AO970725	AO970725	RPCI-23-3	C 260	18	3.2	579	218	AZ257423	AZ257423	RPCI-23-1
C 188	18	3.2	491	218	AZ255121	AZ255121	RPCI-23-1	C 261	18	3.2	580	222	AZ469583	AZ469583	RPCI-23-3
C 189	18	3.2	492	215	AZ016946	AZ016946	RPCI-23-2	C 262	18	3.2	582	122	AW970853	AW970853	EST382936
C 190	18	3.2	492	215	AZ040934	AZ040934	RPCI-23-2	C 263	18	3.2	582	221	AZ403840	AZ403840	IM0171N24
C 191	18	3.2	494	219	AZ304740	AZ304740	IM0004M19	C 264	18	3.2	583	106	AU044979	AU044979	IM0044979
C 192	18	3.2	495	214	AO986626	AO986626	RPCI-23-3	C 265	18	3.2	584	221	AZ031354	AZ031354	RPCI-23-3
C 193	18	3.2	495	216	AZ089856	AZ089856	RPCI-23-7	C 266	18	3.2	584	225	AZ407478	AZ407478	RPCI-23-3
C 194	18	3.2	496	220	AZ350511	AZ350511	IM00088P02	C 267	18	3.2	585	215	AZ028612	AZ028612	RPCI-23-3
C 195	18	3.2	496	219	AZ317256	AZ317256	IM0035L13	C 268	18	3.2	585	215	AZ032801	AZ032801	RPCI-23-3
C 196	18	3.2	497	104	A1968179	A1968179	wu14a09.x	C 269	18	3.2	585	226	AZ747516	AZ747516	RPCI-24-9
C 197	18	3.2	499	24	A1762324	A1762324	*997a03.x	C 270	18	3.2	586	222	AZ475088	AZ475088	IM0293008A
C 198	18	3.2	499	226	AZ723956	AZ723956	RPCI-24-6	C 271	18	3.2	587	215	AZ056228	AZ056228	RPCI-23-4
C 199	18	3.2	502	224	AZ616510	AZ616510	IM0446C30	C 272	18	3.2	588	226	AZ697723	AZ697723	RPCI-23-2
C 200	18	3.2	503	213	AO928048	AO928048	RPCI-23-2	C 273	18	3.2	588	226	AZ721802	AZ721802	RPCI-24-1
C 201	18	3.2	503	226	AZ705395	AZ705395	RPCI-23-2	C 274	18	3.2	593	220	AZ48154	AZ48154	IM0084U05
C 202	18	3.2	504	214	AZ003188	AZ003188	RPCI-23-3	C 275	18	3.2	593	220	AZ385324	AZ385324	IM0143ET3
C 203	18	3.2	505	216	AZ117295	AZ117295	RPCI-23-4	C 276	18	3.2	593	227	B67184	B67184	CPe00008A
C 204	18	3.2	505	224	AZ599821	AZ599821	IM0416D24	C 277	18	3.2	594	221	AZ440149	AZ440149	IM0231002
C 205	18	3.2	506	217	AZ162559	AZ162559	SP-0072.A	C 278	18	3.2	595	226	AZ751126	AZ751126	RPCI-24-8
C 206	18	3.2	507	102	AZ595692	AZ595692	IM0408A05	C 279	18	3.2	596	221	AZ434012	AZ434012	RPCI-220N12
C 207	18	3.2	508	102	A1816914	A1816914	wj35b08.x	C 280	18	3.2	597	222	AZ489136	AZ489136	IM0319H16
C 208	18	3.2	509	214	AO994236	AO994236	RPCI-23-3	C 281	18	3.2	599	215	AZ035299	AZ035299	RPCI-23-2
C 209	18	3.2	509	216	AZ110671	AZ110671	RPCI-23-4	C 282	18	3.2	599	221	AZ398494	AZ398494	IM0163J22
C 210	18	3.2	514	216	AZ118513	AZ118513	RPCI-23-4	C 283	18	3.2	599	226	AZ706200	AZ706200	RPCI-23-2
C 211	18	3.2	515	215	AZ068592	AZ068592	RPCI-23-9	C 284	18	3.2	601	218	AZ255628	AZ255628	RPCI-23-1
C 212	18	3.2	516	218	AZ262631	AZ262631	RPCI-23-8	C 285	18	3.2	601	220	AZ391959	AZ391959	RPCI-23-1
C 213	18	3.2	517	218	AZ236841	AZ236841	RPCI-23-8	C 286	18	3.2	602	220	AZ358517	AZ358517	RPCI-23-1
C 214	18	3.2	518	8	AA517196	AA517196	vh86c03.r	C 287	18	3.2	602	224	AZ607310	AZ607310	IM0429M09
C 215	18	3.2	519	225	AZ653249	AZ653249	IM0526O13	C 288	18	3.2	602	226	AZ715640	AZ715640	RPCI-24-1
C 216	18	3.2	520	148	BF433198	BF433198	7959c09.x	C 289	18	3.2	602	226	AZ715640	AZ715640	RPCI-24-1
C 217	18	3.2	520	218	AZ233277	AZ233277	RPCI-23-5	C 290	18	3.2	604	223	AZ513174	AZ513174	IM0359K07
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C 220	18	3.2	524	167	BE463995	BE463995	hy19608.x	C 293	18	3.2	608	224	AZ607461	AZ607461	IM0429K19
C 221	18	3.2	525	213	AO930643	AO930643	RPCI-23-2	C 294	18	3.2	609	226	AZ719905	AZ719905	RPCI-24-1
C 222	18	3.2	525	221	AZ397270	AZ397270	IM0162K10	C 295	18	3.2	608	215	AZ034858	AZ034858	RPCI-23-2
C 223	18	3.2	529	224	AZ610217	AZ610217	IM0435F24	C 296	18	3.2	611	219	AZ297904	AZ297904	RPCI-23-9
C 224	18	3.2	531	157	779944	779944	vh85b11.s1	C 297	18	3.2	615	222	AZ451955	AZ451955	IM0251L05
C 225	18	3.2	531	214	AZ005985	AZ005985	RPCI-23-3	C 298	18	3.2	615	226	AZ728470	AZ728470	RPCI-24-8
C 226	18	3.2	532	216	AZ099345	AZ099345	RPCI-23-4	C 299	18	3.2	616	221	AZ415838	AZ415838	IM0190K11
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C 228	18	3.2	536	143	BF061874	BF061874	7K68c02.x	C 301	18	3.2	618	221	AZ439925	AZ439925	IM0230G18
C 229	18	3.2	537	226	AZ719267	AZ719267	RPCI-24-1	C 302	18	3.2	621	226	AZ749215	AZ749215	RPCI-24-1
C 230	18	3.2	538	219	AZ299649	AZ299649	RPCI-23-1	C 303	18	3.2	622	225	AZ649140	AZ649140	IM0518B09
C 231	18	3.2	538	223	AZ555866	AZ555866	RPCI-23-2	C 304	18	3.2	622	225	AZ653208	AZ653208	IM0526G14
C 232	18	3.2	539	222	AZ473920	AZ473920	IM0289L02	C 305	18	3.2	623	222	AZ468939	AZ468939	IM0282N08
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C 235	18	3.2	544	222	AZ500560	AZ500560	IM0339D01	C 308	18	3.2	626	226	AZ731119	AZ731119	RPCI-24-1
C 236	18	3.2	546	216	AZ085223	AZ085223	RPCI-23-2	C 309	18	3.2	629	219	AZ322853	AZ322853	IM0044G10
C 237	18	3.2	548	220	AZ348522	AZ348522	IM0085C11	C 310	18	3.2	631	216	AZ098314	AZ098314	RPCI-23-1

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319	18	3.2	643	226	A2742169	RPCT-24-6	392	17	3.1	130	10	AA675452	AA675452	UT-R-B52
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330	18	3.2	654	219	A2037109	RPCT-23-2	403	17	3.1	197	17	A1166537	A1166537	xylem.est
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346	18	3.2	672	221	A2445765	1M0241D21	419	17	3.1	251	22	A1578976	A1578976	UI-R-AA0-
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354	18	3.2	694	221	A2409638	1M0181P16	427	17	3.1	260	29	AV360256	AV360256	AV360256
355	18	3.2	696	219	A2315318	1M0032D03	428	17	3.1	263	202	AQ103434	AQ103434	HS-3058_B
356	18	3.2	700	224	A2615032	1M0444H08	429	17	3.1	265	27	AV285089	AV285089	AV285089
357	18	3.2	701	220	A2368570	1M0118P11	430	17	3.1	267	162	BE100937	BE100937	UI-R-BJ1-
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369	18	3.2	744	221	A2446569	1M0243K02	442	17	3.1	277	138	BE690100	BE690100	u64c11.y
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      AM177132 CM1-CT012
      AO603963 HS_2136_A
      AA766335 ca31b12.s
      AM005139 wv80b11.x
      AM05404 y05d04.s1
      C61709 C61709.Yuji
      C63503 C63503.Yuji
      AM193056 x169f06.x
      AA029964 zK10h10.s
      AO098350 HS_3046_A
      AA244309 nc06c09.r
      AO081776 RPTC11-55
      A1167222 ok28h12.x

      ALIGNMENTS

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        pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
        Soares, M.B. 'Normalization and subtraction: two
        approaches to facilitate gene discovery', Genome Research
        6:791-806, 1996. The first strand synthesis used a
        NotI-dT18 primer; double stranded cDNAs were ligated to
        EcoRI adapters, digested with NotI, and directionally
        cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
        The library contained approximately 7.2 x 10^5
        recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT
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ORIGIN

Query Match
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  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 327 TTTCTTTCCATTACAACTGA 347

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  REFERENCE 1 (bases 1 to 745)
    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
    Kellier,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
    Hood,L.
  TITLE Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE 95380589
  COMMENT Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
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      /db_xref="taxon:9606"
      /clone="Plate-2229 Col=7 Row=M"

```

```

FEATURES
  source
    /clone_lib="CIT Approved Human Genomic Sperm Library D"
    /sex="male"
    /note="Organ: sperm; Vector: pBelOAc11; BAC clones in
    E-Coli DH10B"

BASE COUNT
  252 a 132 c 101 g 245 t 15 others

ORIGIN

Query Match
  Best Local Similarity 100.0%; Score 21; DB 203; Length 745;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 TAAATTTATTTCTCAGCTTTT 55
    |||||
Db 136 TAAATTTATTTCTCAGCTTTT 156

RESULT 3
  LOCUS BE072277 225 bp mRNA EST 09-JUN-2000
  DEFINITION QV4-BT0536-281299-060-C03 BT0536 Homo sapiens cDNA, mRNA sequence.
  accession BE072277
  VERSION BE072277.1 GI:8418134
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  REFERENCE 1 (bases 1 to 225)
    Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Britones,M.R.,
    Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
    Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
    Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
    ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
    Simpson,A.J.
  TITLE Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE 20202663
  COMMENT Contact: Simpson A.J.G.
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brazil
  Tel: +55-11-2704922
  Fax: +55-11-2707001
  Email: asimpson@ludwig.org.br
  This sequence was derived from the FAPESP/LICR Human Cancer Genome
  Project. This entry can be seen in the following URL
  (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6tz-QV4-BT0536-281
  299-060-C03&ts=1999-12-28&tl=1)
  Seg primer: puc 18 forward
  High quality sequence stop: 225.
  Location/Qualifiers
    1..225
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone_lib="BT0536"
      /dev_stage="Adult"
      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
      SmaI; A mini-library was made by cloning products derived
      from ORESTES PCR (U.S. Letters Patent Application No. 196
      ,716 - Ludwig Institute for Cancer Research) profiles
      into the pUC 18 vector. Reverse transcription of tissue
      mRNA and cDNA amplification were performed under low
      stringency conditions."

BASE COUNT
  75 a 38 c 33 g 79 t

ORIGIN

Query Match
  Best Local Similarity 100.0%; Score 20; DB 162; Length 225;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 143 CTGTTAAAGCAGCTTGCT 162
 DB 32 CTGTTAAAGCAGCTTGCT 51

RESULT 4
 BF906208 404 bp mRNA EST 18-JAN-2001
 LOCUS IL3-MT0267-291200-426-G10 MT0267 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF906208
 ACCESSION BF906208.1 GI:12297667
 VERSION EST.
 KEYWORDS human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 404)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,
 M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J. J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL 20202663
 MEDLINE
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?IL3=IL3&IL2=IL3-MT0267-291200-426-G10&IL3=2000-12-29&IL4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 276.

FEATURES
 source
 Location/Qualifiers
 1..404
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MT0267"
 /dev_stage="Adult"
 /note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 99 a 118 c 88 g 99 t
 ORIGIN

Query Match 3.6%; Score 20; DB 170; Length 404;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GCTTCTTCCCATTAACA 69
 DB 26 GCTTCTTCCCATTAACA 7

RESULT 5
 AZ502214 667 bp DNA GSS 05-OCT-2000
 LOCUS 1M0341J01R Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone U06C1M0341J01 R, DNA sequence.

ACCESSION AZ502214
 VERSION AZ502214.1 GI:10683626
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 667)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0341 row: J column: 01
 Seq primer: CACACAGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 667.

FEATURES
 source
 Location/Qualifiers
 1..667
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0341J01"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 175 a 155 c 122 g 214 t 1 others
 ORIGIN

Query Match 3.6%; Score 20; DB 223; Length 667;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATATGATTAATTTATTC 46
 DB 612 GGATATGATTAATTTATTC 593

RESULT 6
 AO854708 688 bp DNA GSS 12-MAY-2000
 LOCUS CpG2172A CptOWAgDNA1 Cryptosporidium parvum genomic, DNA sequence.
 DEFINITION

ACCESSION A0854708
 VERSION A0854708.1 GI:6205165
 KEYWORDS GSS.
 SOURCE Cryptosporidium parvum.
 ORGANISM Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporididae; Cryptosporidium.
 REFERENCE 1 (bases 1 to 688)
 Strong, W.B. and Nelson, R.G.
 Preliminary profile of the *Cryptosporidium parvum* genome: an
 expressed sequence tag and genome survey sequence analysis
 Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
 20183851
 JOURNAL MEDLINE
 COMMENT Contact: Nelson, R. G.
 Depts. of Medicine & Pharmaceutical Chemistry
 San Francisco General Hospital-University of California, San
 Francisco
 Box 0811, San Francisco, CA 94143-0811, USA
 Tel: 415 206 8846
 Fax: 415 206 3353
 Email: malarial@lisa.ucsf.edu
 For Annotation Data see <http://medsfh.ucsf.edu/id/CPTags/home.html>
 Seq primer: M13(-21) forward
 Class: Shotgun.
 FEATURES
 source
 1..688
 /organism="Cryptosporidium parvum"
 /strain="IOWA"
 /db_xref="taxon:5807"
 /clone_lib="CPIOWAGDNA1"
 /lab_host="E. coli XL2 Blue MRF"
 /note="Vector: pBluescript II (SK-); Site:1: EcoRV; C.
 parvum (IOWA isolate) genomic DNA was hydrodynamically
 sheared to produce fragments having a light size
 distribution between 2-4 kb by Dr. Yvonne Thorsen of
 the Stanford DNA Sequencing and Technology Center
 (<http://sequence-www.stanford.edu/group/techdev/shear.htm>
). The randomly sheared gDNA was chromatographed on
 Sephacryl S-400 to remove any small fragments and DNA
 eluting in the void volume was subcloned into an EcoR
 V-digested, alkaline phosphatase-treated pBluescript II
 (SK-) vector and transformed into E. coli strain XL2 Blue
 MRF'. Recombinant clones from the first plating of the
 library were selected for sequence analysis using T3 and
 T7 primers."

BASE COUNT 238 a 106 c 113 g 231 t
 ORIGIN

Query Match 3.6%; Score 20; DB 212; Length 688;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 ATATAGACAGTATTTTAAA 537
 ||||||||||||||||||||
 Db 274 ATATAGACAGTATTTTAAA 293

RESULT 7
 CNS01VPE 771 bp DNA GSS 12-MAY-2000
 LOCUS Tetradon nigriviridis genome survey sequence T7 end of clone
 DEFINITION 199G15 of library G from Tetradon nigriviridis, genomic survey
 sequence.
 ACCESSION AL169403
 VERSION AL169403.1 GI:7807460
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigriviridis.
 ORGANISM Tetradon nigriviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
 Holacanthopterygii; Acanthopterygii; Percomorpha;

REFERENCE 1
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
 Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
 Weissenbach, J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigriviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 771)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
 Saurin, W. and Weissenbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetradon nigriviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 771)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large
 genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetradon>.

FEATURES
 source
 1..771
 /organism="Tetradon nigriviridis"
 /db_xref="taxon:99883"
 /clone_lib="199G15"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG199A0808LP1-end : T7"
 BASE COUNT 168 a 194 c 193 g 211 t 5 others
 ORIGIN

Query Match 3.6%; Score 20; DB 230; Length 771;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TAGAGTTAAGAGCTTTTAA 259
 ||||||||||||||||||||
 Db 97 TAGAGTTAAGAGCTTTTAA 78

RESULT 8
 CNS03B2I 983 bp DNA GSS 15-MAY-2000
 LOCUS Tetradon nigriviridis genome survey sequence T7 end of clone
 DEFINITION 013G02 of library G from Tetradon nigriviridis, genomic survey
 sequence.
 ACCESSION AL237159
 VERSION AL237159.1 GI:7896294
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigriviridis.
 ORGANISM Tetradon nigriviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
 Holacanthopterygii; Acanthopterygii; Percomorpha;
 Tetradontiformes; Tetradontoidae; Tetradontidae; Tetradon.
 REFERENCE 1 (bases 1 to 983)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
 Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
 Weissenbach, J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigriviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 983)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
 Saurin, W. and Weissenbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetradon nigriviridis DNA sequence
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 983)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..983
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="013602"
/clone_lib="G"
/note="Genoscope sequence ID : COBG013BD01LPI-end : T7"
BASE COUNT 246 a 251 c 235 g 248 t 3 others
ORIGIN

Query Match 3.6%; Score 20; DB 230; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AATATATGGAATATGCAATT 125
|||||
Db 161 AATATATGGAATATGCAATT 142

RESULT 9
CNS0421Y 1016 bp DNA GSS 18-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone
DEFINITION 075F19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL270943
VERSION AL270943.1 GI:7992890
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 1016)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1016)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Barnot,A., Fizames,C., Wincker,P., Brotier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1016)
Genoscope.
TITLE Direct Submission
AUTHORS Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..1016
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/db_xref="taxon:99883"
/clone="075F19"
/clone_lib="G"
/note="Genoscope sequence ID : COBG075C10SP1-end :

BASE COUNT PUC-Orl"
ORIGIN 261 a 238 c 264 g 244 t 9 others

Query Match 3.6%; Score 20; DB 231; Length 1016;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AATATATGGAATATGCAATT 125
|||||
Db 761 AATATATGGAATATGCAATT 780

RESULT 10
CNS03009 1019 bp DNA GSS 17-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone
DEFINITION 043M02 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL253602
VERSION AL253602.1 GI:7974614
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 1019)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1019)
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,
Barnot,A., Fizames,C., Wincker,P., Brotier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1019)
Genoscope.
TITLE Direct Submission
AUTHORS Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..1019
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="043M02"
/clone_lib="G"
/note="Genoscope sequence ID : COBG043BG01SP1-end :

BASE COUNT 221 a 265 c 250 g 276 t 7 others
ORIGIN

Query Match 3.6%; Score 20; DB 231; Length 1019;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AATATATGGAATATGCAATT 125
|||||
Db 36 AATATATGGAATATGCAATT 17

RESULT	11
LOCUS	AV374815
DEFINITION	AV374815 RIKEN full-length enriched, adult male cecum Mus musculus cDNA clone g130016G16 3' similar to X1361 Mouse mRNA for elongation factor 1-alpha (EF-1-alpha), mRNA sequence.
ACCESSION	AV374815
VERSION	AV374815.1
KEYWORDS	GI:6422462
SOURCE	EST.
ORGANISM	house mouse. Mus musculus
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 233)
AUTHORS	Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Harai, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, D., Kikuchi, N., Kojima, Y., Koya, S., Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugihara, Y., Suzuki, H., Suzuki, K., Takahashi, F., Tateno, M., Tomioka, N., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshida, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
TITLE	RIKEN Mouse ESTs (Kono, H., et al. 1999)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Yoshihide Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel.: +81-298-36-9013 Fax: +81-298-36-9098 Email: genome-res@rtc.riken.go.jp/ URL: http://genome.rtc.riken.go.jp/ Sasaki, N., Izawa, M., Watabiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsuai, T., Akiyama, T., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details. Location/Qualifiers 1..233 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_id="g130016G16" /clone_lib="RIKEN full-length enriched, adult male cecum" /sex="male" /tissue_type="cecum" /dev_stage="adult" /lab_host="DH10B" /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15' GAAGACAGACAGATCCAGACGCCTTTTGTGGTTTTTNN 3', cDNA was prepared by using triethanol thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization

Query Match	3.4%: Score 19; DB 29; Length 233;	Best Local Similarity 100.0%; Pred. No. 18;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
<p>Query Match</p> <p>Best Local Similarity 100.0%; Pred. No. 18;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>to Rot = 10.0 and subtracction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGACGATTCGAGTAAATTAATTAATCCCCCCCCCC 3'. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"</p>	<p>BASE COUNT</p> <p>76 a 33 c 40 g 84 t</p>	<p>ORIGIN</p>
<p>Query Match</p> <p>Best Local Similarity 100.0%; Pred. No. 18;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>3.4%: Score 19; DB 29; Length 233;</p> <p>Best Local Similarity 100.0%; Pred. No. 18;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>BASE COUNT</p> <p>76 a 33 c 40 g 84 t</p>	<p>ORIGIN</p>
<p>Query Match</p> <p>Best Local Similarity 100.0%; Pred. No. 18;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>3.4%: Score 19; DB 174; Length 265;</p> <p>Best Local Similarity 100.0%; Pred. No. 18;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>BASE COUNT</p> <p>79 a 72 c 43 g 71 t</p>	<p>ORIGIN</p>

DB	252	ATGCTTGATACATTTCT	234	
RESULT	13			
LOCUS	X61840			
DEFINITION	MUSTSG129X lambda uni-ZAP II Mus musculus cDNA clone Tsg129X, mRNA sequence.			
ACCESSION	X61840			
VERSION	X61840.1			
KEYWORDS	GI:54948			
SOURCE	EST.			
ORGANISM	house mouse.			
	Mus musculus			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 288)			
TITLE	Hoog, C.			
JOURNAL	Isolation of a large number of novel mammalian genes by a differential cDNA library screening strategy			
MEDLINE	Nucleic Acids Res. 19, 6123-6127 (1991)			
COMMENT	92066457			
	Contact: C. Hoog			
	Dept. of Molecular Genetics			
	Karolinska Institutet			
	Box 60400, 10401 Stockholm, SWEDEN.			
FEATURES	Location/Qualifiers			
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	/note="Vector: Lambda uni-ZAP II; Testis tissue.			
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ORIGIN				
Query Match	3.4%; Score 19; DB 159; Length 288;			
Best Local Similarity	100.0%; Pred. No. 18;			
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	311 ATGCTTGATACATTTCT 329			
Db	72 ATGCTTGATACATTTCT 90			
RESULT	14			
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DEFINITION	BB266564 RIKEN full-length enriched, 10 days neonate cortex Mus musculus cDNA A830026E08 3', mRNA sequence.			
ACCESSION	BB266564			
VERSION	BB266564.1			
KEYWORDS	GI:8963026			
SOURCE	EST.			
ORGANISM	house mouse.			
	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 291)			
AUTHORS	Konno, H., Aitawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, T., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owo, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaoka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.			
TITLE	RIKEN Mouse ESTs (Konno, H., et al.)			

JOURNAL COMMENT

Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Email: genome-res@rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover.A., Itoh.M., Nagasaka.S., Sasakawa.
.N., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Thermotabilization and thermocactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (27), 520-524 (1998)
Itoh.M., Katsunari.T., Akiyama.J., Shibata.K., Itawa.M., Kawai.J.,
Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M., Okazaki.
.Y. and Hayashizaki.Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES
SOURCE

Location/Qualifiers
1..291
/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched, 10 days neonate
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/note="Site_1: Sali; Site_2: BamHI; CDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGGAGGAGAAGATCCAAAGACGCTCTTTTTCCTTTTTTTTNN 3'], cDNA was
prepared by using trehalase thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adaptor of
sequence [5' GAGGAGGAGATTCTCGACTTAATAATATATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pluscript KS(+) after bulk excision from Lambda
FLC 1."

BASE COUNT 79 a 60 c 53 g 99 t

ORIGIN

Query Match 3.4%; Score 19; DB 129; Length 291;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 ACATGCTGTAAACGAGT 156
|||||
DB 274 ACATGCTGTAAACGAGT 256

RESULT 15
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LOCUS BF460484/C
DEFINITION UI-M-CG0p-bmd-b-06-0-ui.s1 NIH BMAP RetL S2 Mus musculus cDNA clone
accession BF460484
VERSION BF460484.1 GI:11529641

KEYWORDS

EST,
house mouse,
Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 302)

AUTHORS

Bonafide,M.F., Lennon,G. and Soares,M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

COMMENT

Contact: Chin, H

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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
retina tissue cDNA library preparation: M.B. Soares Lab Clone
distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
GENETICS. It should be noted that Bento Soares is generating a
small number of additional specialized non-redundant arrays of BMAP
cDNAs whose availability will be considered under appropriate and
limited collaborative arrangements The following repetitive
elements were found in this cDNA sequence: 1-21,
>AT_rich#low_complexity
Seq primer: M13 Forward
POLYA-Yes.

FEATURES

source

Location/Qualifiers

1..302
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/lab_host="DH10B (Life Technologies)"
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NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIH_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTGAGCGGCAC"

BASE COUNT

86 a 83 c 51 g 82 t

ORIGIN

Query Match

3.4%; Score 19; DB 148; Length 302;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 311 ATGGTGGATACATTTCCT 329

Db 266 ATGCTTGATACATTTCCT 248

Search completed: May 31, 2001, 01:25:10
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